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      Le Page, Richard WF
      Wells, Jeremy M
      Hanniffy, Sean B
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Asp Gln Glu Asp Ser Val Leu Lys Ala Val Tyr His Gly Glu Thr Ser 100 105 110

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Lys Arg Leu Ala Gln Thr Ile Gln Phe Thr Glu Lys Ile Asp Glu Ala 145 150 155 160

Lys Glu Asn Lys Lys Phe Ile Gln Thr Ile Ala Ala Gly Ala Leu Gly 165 170 175

Phe Phe Leu Tyr Met Ile Leu Ile Thr Tyr Ala Gly Val Thr Ala Gln 180 185 190

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Leu Asp His Leu Gly Asp Ala Ile Ser Leu Asn Thr Leu Leu Phe Ile 260 265 270

Leu Ile Ser Leu Phe Met Tyr Val Val Leu Ala Ala Phe Leu Gly Ser 275 280 285

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- Lys Lys Asn Gln Ala Ser Gly Phe Asn Leu Gly Val Lys His Ser Val
 100 105 110
- Gly Asp Leu Ile Leu Lys Ile Asp Ala His Ser Lys Val Thr Glu Thr 115 120 125
- Phe Val Met Asn Asn Val Ala Ile Ile Gln Gln Gly Glu Phe Val Cys 130 135 140
- Gly Gly Pro Arg Pro Thr Ile Val Glu Gly Lys Gly Lys Trp Ala Glu 145 150 155 160
- Thr Leu His Leu Val Glu Glu Asn Met Phe Gly Ser Ser Ile Ala Asn 165 170 175
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- Met Tyr Lys Arg Glu Val Phe Gln Lys Val Gly Leu Val Asn Glu Gln
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- Leu Gly Arg Thr Glu Asp Asn Asp Ile His Tyr Arg Ile Arg Glu Tyr 210 215 220
- Gly Tyr Lys Ile Arg Tyr Ser Pro Ser Ile Leu Ser Tyr Gln Tyr Ile 225 230 235 240
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Thr Thr Leu Glu Glu Ala Arg Pro Ala Ile Ser Pro Ser Ser Pro Asn 165 170 175

Ile Lys Arg Asn Thr Leu Ile Gly Phe Leu Ala Gly Val Ile Gly Thr
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Arg Ala Asp His Val Phe Asp Gly Asp Leu Ser Asp Tyr Asp Met Ile 50 60

Val Leu Pro Gly Gly Met Pro Gly Ser Ala His Leu Arg Asp Asn Gln 65 70 75 80

Thr Leu Ile Gln Glu Leu Gln Ser Phe Glu Gln Glu Gly Lys Lys Leu 85 90 95

Ala Ala Ile Cys Ala Ala Pro Ile Ala Leu Asn Gln Ala Glu Ile Leu 100 105 110

Lys Asn Lys Arg Tyr Thr Cys Tyr Asp Gly Val Gln Glu Gln Ile Leu 115 120 125

Asp Gly His Tyr Val Lys Glu Thr Val Val Val Asp Gly Gln Leu Thr 130 135 140

Thr Ser Arg Gly Pro Ser Thr Ala Leu Ala Phe Ala Tyr Glu Leu Val 145 150 155 160

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- Gly Lys Glu Val Glu Asn Leu Glu Ile Thr Leu His Gln His Thr Leu 65 70 75 80
- Thr Ile Thr Asp Ser Phe Asp Asp Gln Ile His Ile Ser Tyr His Pro
 85 90 95
- Ser Leu Ser Ala His His Asp Leu Ile Thr Asn Gln Asn Asp Arg Thr 100 105 110
- Leu Ser Leu Thr Asp Lys Lys Leu Ser Glu Thr Pro Phe Leu Ser Ser 115 120 125
- Gly Ile Gly Gly Ile Leu His Ile Ala Ser Ser Tyr Ser Ser Arg Phe 130 135 140
- Glu Glu Val Ile Leu Arg Leu Pro Lys Gly Arg Thr Leu Lys Gly Ile 145 150 155 160
- Asn Ile Ser Ala Asn Arg Gly Gln Thr Thr Ile Ile Asn Ala Ser Leu 165 170 175
- Glu Asn Ala Thr Leu Asn Thr Asn Ser Tyr Ile Leu Arg Ile Glu Gly
 180 185 190
- Ser Arg Ile Lys Asn Ser Lys Leu Thr Thr Pro Asn Ile Val Asn Ile 195 200 205
- Phe Asp Thr Val Leu Thr Asp Ser Gln Leu Glu Ser Thr Glu Asn His 210 215 220
- Phe His Ala Glu Asn Ile Gln Val His Gly Lys Val Glu Leu Thr Ala 225 230 235 240
- Lys Asp Tyr Leu Arg Ile Ile Leu Asp Gln Lys Glu Ser Ĝln Arg Ile 245 250 255
- Asn Trp Asp Ile Ser Ser Asn Tyr Gly Ser Ile Phe Gln Phe Thr Arg
 260 265 270
- Glu Lys Pro Glu Ser Arg Gly Thr Glu Leu Ser Asn Pro Tyr Lys Thr 275 280 285
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Glu Ser Pro Tyr Ile Pro Asp Gln Ala Pro Lys Ser Arg Asp Lys Trp

Lys Glu Gln Val Leu Asp Phe Trp Ser Trp Leu Val Glu Ala Ile Lys

135

145 150 155 160

Ser Pro Thr Ser Lys Leu Glu Thr Ser Ile Thr His Ser Tyr Thr Ala 165 170 175

Phe Leu Leu Ile Leu Phe Ser Ala Ser Ser Phe Phe Phe Ser Ile 180 185 190

Tyr His Ile Lys His Ala Tyr Tyr Gly His Ile Ala Ser Ile Asn Ser 195 200 205

Arg Phe Pro Glu Gln Leu Ala Pro Leu Thr Leu Phe Ser Ile Ile Ser 210 215 220

Ile Leu Val Ala Thr Thr Leu Phe Phe Phe Ser Phe Leu Leu Gly Ser 225 230 235 240

Phe Val Val Arg Arg Phe Ile His Gln Glu Lys Asp Trp Thr Leu Asp 245 250 255

Lys Val Leu Gln Gln Tyr Ser Gln Leu Leu Ala Ile Pro Ile Ser Ser 260 265 270

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Lys Glu Val Glu Asn Leu Glu Ile Thr Leu His Gln His Thr Leu Thr
85 90 95

Ile Thr Asp Ser Phe Asp Asp Gln Ile His Ile Ser Tyr His Pro Ser 100 105 110

Leu Ser Ala His His Asp Leu Ile Thr Asn Gln Asn Asp Arg Thr Leu 115 120 125

Ser Leu Thr Asp Lys Lys Leu Ser Glu Thr Pro Phe Leu Ser Ser Gly 130 135 140

Ile Gly Gly Ile Leu His Ile Ala Ser Ser Tyr Ser Ser Arg Phe Glu 145 150 155 160

Glu Val Ile Leu Arg Leu Pro Lys Gly Arg Thr Leu Lys Gly Ile Asn 165 170 175

Ile Ser Ala Asn Arg Gly Gln Thr Thr Ile Ile Asn Ala Ser Leu Glu 180 185 190

Asn Ala Thr Leu Asn Thr Asn Ser Tyr Ile Leu Arg Ile Glu Gly Ser 195 200 205

Arg Ile Lys Asn Ser Lys Leu Thr Thr Pro Asn Ile Val Asn Ile Phe 210 215 220

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His Ala Glu Asn Ile Gln Val His Gly Lys Val Glu Leu Thr Ala Lys 245 250 255

Asp Tyr Leu Arg Ile Ile Leu Asp Gln Lys Glu Ser Gln Arg Ile Asn 260 265 270

Trp Asp Ile Ser Ser Asn Tyr Gly Ser Ile Phe Gln Phe Thr Arg Glu

275 280 285

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Lys Ser Leu Val Ser Ile Ile Ser Pro Ser Ser Gly Arg Ile Leu Val

Asp Gly Gln Glu Leu Ser Glu Asn Arg Leu Ala Ile Lys Arg Lys Ile 50 55 60

Gly Tyr Val Ala Asp Ser Pro Asp Leu Phe Leu Arg Leu Thr Ala Asn 65 70 75 80

Glu Phe Trp Glu Leu Ile Ala Ser Ser Tyr Asp Leu Ser Arg Ser Asp 85 90 95

Leu Glu Ala Ser Leu Ala Arg Leu Leu Asn Val Phe Asp Phe Ala Glu 100 105 110

Asn Arg Tyr Gln Val Ile Glu Thr Leu Ser His Gly Met Arg Gln Lys 115 120 125

Val Phe Val Ile Gly Ala Leu Leu Ser Asp Pro Asp Ile Trp Val Leu 130 135 140

Asp Glu Pro Leu Thr Gly Leu Asp Pro Gln Ala Ala Phe Asp Leu Lys 145 150 155 160

Gln Met Met Lys Glu His Ala Gln Lys Gly Lys Thr Val Leu Phe Ser 165 170 175

Thr His Val Leu Glu Val Ala Glu Gln Val Cys Asp Arg Ile Ala Ile 180 185 190

Leu Lys Cly His Leu Ile Tyr Cys Gly Lys Val Glu Asp Leu Arg
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Lys Asp His Pro Asp Gln Ser Leu Glu Ser Ile Tyr Leu Ser Leu Ala 210 215 220

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Gln Lys Ser Glu Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly 50 55 60

Ile Gln Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val 65 70 75 80

Thr Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr 85 90 95

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Leu Lys Asp Ala Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile 115 120 125

Lys Val Asp Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala 130 135 140

Asp Asn Val Arg Thr Lys Asp Glu Ile Asn Arg Gln Lys Gln Glu His 145 150 155 160

Val Lys Asp Asn Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser 165 170 175

- Gln Gly Arg Tyr Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp 180 185 190
- Ile Ile Glu Asp Thr Gly Asn Ala Tyr Ile Val Pro His Gly Gly His 195 200 205
- Tyr His Tyr Ile Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala 210 215 220
- Ala Lys Ala His Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser 225 230 235 240
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- Ser Thr Ser Lys Pro Ala Asn Lys Ser Glu Asn Leu Gln Ser Leu Leu 260 265 270
- Lys Glu Leu Tyr Asp Ser Pro Ser Ala Gln Arg Tyr Ser Glu Ser Asp 275 280 285
- Gly Leu Val Phe Asp Pro Ala Lys Ile Ile Ser Arg Thr Pro Asn Gly 290 295 300
- Val Ala Ile Pro His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Lys 305 310 315 320
- Leu Ser Ala Leu Glu Glu Lys Ile Ala Arg Met Val Pro Ile Ser Gly 325 330 335
- Thr Gly Ser Thr Val Ser Thr Asn Ala Lys Pro Asn Glu Val Val Ser 340 345 350
- Ser Leu Gly Ser Leu Ser Ser Asn Pro Ser Ser Leu Thr Thr Ser Lys 355 360 365
- Glu Leu Ser Ser Ala Ser Asp Gly Tyr Ile Phe Asn Pro Lys Asp Ile 370 375 380
- Val Glu Glu Thr Ala Thr Ala Tyr Ile Val Arg His Gly Asp His Phe 385 390 395 400
- His Tyr Ile Pro Lys Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro Asn 405 410 415
- Asn Ser Leu Ala Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr 420 425 430
- Ser His Glu Lys His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg 435 440 445
- Ile Ile Ala Glu Asp Glu Ser Gly Phe Val Met Ser His Gly Asp His
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Gly Ser Tyr Thr Ala Leu Ile Gly His Thr Gly Ser Gly Lys Ser Thr
         35
Ile Leu Gln Leu Leu Asn Gly Leu Leu Val Pro Ser Gln Gly Ser Val
Arq Val Phe Asp Thr Leu Ile Thr Ser Thr Ser Lys Asn Lys Asp Ile
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                                         75
Arg Gln Ile Arg Lys Gln Val Gly Leu Val Phe Gln Phe Ala Glu Asn
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Asn Phe Gly Val Ser Glu Glu Asp Ala Val Lys Thr Ala Arg Glu Lys
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Ala Val Ile Lys Glu Lys Glu Val Val Ser Lys Asn Pro Val Ile Asp

Asn Asn Thr Ser Asn Glu Glu Ala Lys Ile Lys Glu Glu Asn Ser Asn 70 65

Lys Ser Gln Gly Asp Tyr Thr Asp Ser Phe Val Asn Lys Asn Thr Glu 85 90

Asn Pro Lys Lys Glu Asp Lys Val Val Tyr Ile Ala Glu Phe Lys Asp

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Glu Thr Thr Pro Asp Asn Leu Asp Lys Ile Lys Gln Ile Glu Gly Ile 145 150 155 160

Ser Ser Val Glu Arg Ala Gln Lys Val Gln Pro Met Met Asn His Ala 165 170 175

Arg Lys Glu Ile Gly Val Glu Glu Ala Ile Asp Tyr Leu Lys Ser Ile 180 185 190

Asn Ala Pro Phe Gly Lys Asn Phe Asp Gly Arg Gly Met Val Ile Ser 195 200 205

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Ala Pro Asn Ala Gln Ile Phe Ser Tyr Lys Met Tyr Ser Asp Ala Gly 305 310 315

Ser Gly Phe Ala Gly Asp Glu Thr Met Phe His Ala Ile Glu Asp Ser 325 330 335

Ile Lys His Asn Val Asp Val Val Ser Val Ser Ser Gly Phe Thr Gly 340 345 350

Thr Gly Leu Val Gly Glu Lys Tyr Trp Gln Ala Ile Arg Ala Leu Arg 355 360 365

Lys Ala Gly Ile Pro Met Val Val Ala Thr Gly Asn Tyr Ala Thr Ser 370 380

Ala Ser Ser Ser Ser Trp Asp Leu Val Ala Asn Asn His Leu Lys Met 385 390 395 400

Thr Asp Thr Gly Asn Val Thr Arg Thr Ala Ala His Glu Asp Ala Ile

405 410 415

Ala Val Ala Ser Ala Lys Asn Gln Thr Val Glu Phe Asp Lys Val Asn 420 425 430

Ile Gly Glu Ser Phe Lys Tyr Arg Asn Ile Gly Ala Phe Phe Asp 435 440 445

Lys Ser Lys Ile Thr Thr Asn Glu Asp Gly Thr Lys Ala Pro Ser Lys 450 455 460

Leu Lys Phe Val Tyr Ile Gly Lys Gly Gln Asp Gln Asp Leu Ile Gly 465 470 475 480

Leu Asp Leu Arg Gly Lys Ile Ala Val Met Asp Arg Ile Tyr Thr Lys
485 490 495

Asp Leu Lys Asn Ala Phe Lys Lys Ala Met Asp Lys Gly Ala Arg Ala 500 505 510

Ile Met Val Val Asn Thr Val Asn Tyr Tyr Asn Arg Asp Asn Trp Thr 515 520 525

Glu Leu Pro Ala Met Gly Tyr Glu Ala Asp Glu Gly Thr Lys Ser Gln 530 535 540

Val Phe Ser Ile Ser Gly Asp Asp Gly Val Lys Leu Trp Asn Met Ile 545 550 555 560

Asn Pro Asp Lys Lys Thr Glu Val Lys Arg Asn Asn Lys Glu Asp Phe 565 570 575

Lys Asp Lys Leu Glu Gln Tyr Tyr Pro Ile Asp Met Glu Ser Phe Asn 580 585 590

Ser Asn Lys Pro Asn Val Gly Asp Glu Lys Glu Ile Asp Phe Lys Phe 595 600 605

Ala Pro Asp Thr Asp Lys Glu Leu Tyr Lys Glu Asp Ile Ile Val Pro 610 615 620

Ala Gly Ser Thr Ser Trp Gly Pro Arg Ile Asp Leu Leu Leu Lys Pro 625 630 635 640

Asp Val Ser Ala Pro Gly Lys Asn Ile Lys Ser Thr Leu Asn Val Ile 645 650 655

Asn Gly Lys Ser Thr Tyr Gly Tyr Met Ser Gly Thr Ser Met Ala Thr 660 665 670

Pro Ile Val Ala Ala Ser Thr Val Leu Ile Arg Pro Lys Leu Lys Glu 675 680 685

Met Leu Glu Arg Pro Val Leu Lys Asn Leu Lys Gly Asp Asp Lys Ile 690 695 700

Asp Leu Thr Ser Leu Thr Lys Ile Ala Leu Gln Asn Thr Ala Arg Pro

705 / 710 715 720

Met Met Asp Ala Thr Ser Trp Lys Glu Lys Ser Gln Tyr Phe Ala Ser 725 730 735

Pro Arg Gln Gln Gly Ala Gly Leu Ile Asn Val Ala Asn Ala Leu Arg 740 745 750

Asn Glu Val Val Ala Thr Phe Lys Asn Thr Asp Ser Lys Gly Leu Val 755 760 765

Asn Ser Tyr Gly Ser Ile Ser Leu Lys Glu Ile Lys Gly Asp Lys Lys 770 780

Tyr Phe Thr Ile Lys Leu His Asn Thr Ser Asn Arg Pro Leu Thr Phe 785 790 795 800

Lys Val Ser Ala Ser Ala Ile Thr Thr Asp Ser Leu Thr Asp Arg Leu 805 810 815

Lys Leu Asp Glu Thr Tyr Lys Asp Glu Lys Ser Pro Asp Gly Lys Gln 820 825 830

Ile Val Pro Glu Ile His Pro Glu Lys Val Lys Gly Ala Asn Ile Thr 835 840 845

Phe Glu His Asp Thr Phe Thr Ile Gly Ala Asn Ser Ser Phe Asp Leu 850 855 860

Asn Ala Val Ile Asn Val Gly Glu Ala Lys Asn Lys Asn Lys Phe Val 865 870 875 880

Glu Ser Phe Ile His Phe Glu Ser Val Glu Ala Met Glu Ala Leu Asn 885 890 895

Ser Ser Gly Lys Lys Ile Asn Phe Gln Pro Ser Leu Ser Met Pro Leu 900 905 $^{\circ}$ 910

Met Gly Phe Ala Gly Asn Trp Asn His Glu Pro Ile Leu Asp Lys Trp 915 920 925

Ala Trp Glu Glu Gly Ser Arg Ser Lys Thr Leu Gly Gly Tyr Asp Asp 930 935 940

Asp Gly Lys Pro Lys Ile Pro Gly Thr Leu Asn Lys Gly Ile Gly Gly 945 950 955 960

Glu His Gly Ile Asp Lys Phe Asn Pro Ala Gly Val Ile Gln Asn Arg 965 970 975

Lys Asp Lys Asn Thr Thr Ser Leu Asp Gln Asn Pro Glu Leu Phe Ala 980 985 990

Phe Asn Asn Glu Gly Ile Asn Ala Pro Ser Ser Ser Gly Ser Lys Ile 995 1000 1005

Ala Asn Ile Tyr Pro Leu Asp Ser Asn Gly Asn Pro Gln Asp Ala Gln

1010 1015 1020

Leu Glu Arg Gly Leu Thr Pro Ser Pro Leu Val Leu Arg Ser Ala Glu 1025 1030 1035 1040

- Glu Gly Leu Ile Ser Ile Val Asn Thr Asn Lys Glu Gly Glu Asn Gln 1045 1050 1055
- Arg Asp Leu Lys Val Ile Ser Arg Glu His Phe Ile Arg Gly Ile Leu 1060 1065 1070
- Asn Ser Lys Ser Asn Asp Ala Lys Gly Ile Lys Ser Ser Lys Leu Lys 1075 1080 1085
- Val Trp Gly Asp Leu Lys Trp Asp Gly Leu Ile Tyr Asn Pro Arg Gly 1090 1095 1100
- Arg Glu Glu Asn Ala Pro Glu Ser Lys Asp Asn Gln Asp Pro Ala Thr 1105 1110 1115 1120
- Lys Ile Arg Gly Gln Phe Glu Pro Ile Ala Glu Gly Gln Tyr Phe Tyr 1125 1130 1135
- Lys Phe Lys Tyr Arg Leu Thr Lys Asp Tyr Pro Trp Gln Val Ser Tyr
 1140 1145 1150
- Ile Pro Val Lys Ile Asp Asn Thr Ala Pro Lys Ile Val Ser Val Asp 1155 1160 1165
- Phe Ser Asn Pro Glu Lys Ile Lys Leu Ile Thr Lys Asp Thr Tyr His
- Lys Val Lys Asp Gln Tyr Lys Asn Glu Thr Leu Phe Ala Arg Asp Gln 1185 1190 1195 1200
- Lys Glu His Pro Glu Lys Phe Asp Glu Ile Ala Asn Glu Val Trp Tyr 1205 1210 1215
- Ala Gly Ala Ala Leu Val Asn Glu Asp Gly Glu Val Glu Lys Asn Leu 1220 1225 1230
- Glu Val Thr Tyr Ala Gly Glu Gly Gln Gly Arg Asn Arg Lys Leu Asp 1235 1240 1245
- Lys Asp Gly Asn Thr Ile Tyr Glu Ile Lys Gly Ala Gly Asp Leu Arg 1250 1255 1260
- Gly Lys Ile Ile Glu Val Ile Ala Leu Asp Gly Ser Ser Asn Phe Thr 1265 1270 1275 1280
- Lys Ile His Arg Ile Lys Phe Ala Asn Gln Ala Asp Glu Lys Gly Met 1285 1290 1295
- Ile Ser Tyr Tyr Leu Val Asp Pro Asp Gln Asp Ser Ser Lys Tyr Gln
 1300 1305 1310
- Lys Leu Gly Glu Ile Ala Glu Ser Lys Phe Lys Asn Leu Gly Asn Gly

1315 1320 1325

Lys Glu Gly Ser Leu Lys Lys Asp Thr Thr Gly Val Glu His His His 1330 1335 1340

Gln Glu Asn Glu Glu Ser Ile Lys Glu Lys Ser Ser Phe Thr Ile Asp 1345 1350 1355 1360

Arg Asn Ile Ser Thr Ile Arg Asp Phe Glu Asn Lys Asp Leu Lys Lys 1365 1370 1375

Leu Ile Lys Lys Lys Phe Arg Glu Val Asp Asp Phe Thr Ser Glu Thr 1380 1385 1390

Gly Lys Arg Met Glu Glu Tyr Asp Tyr Lys Tyr Asp Asp Lys Gly Asn 1395 1400 1405

Ile Ile Ala Tyr Asp Asp Gly Thr Asp Leu Glu Tyr Glu Thr Glu Lys 1410 1415 1420

Leu Asp Glu Ile Lys Ser Lys Ile Tyr Gly Val Leu Ser Pro Ser Lys 1425 1430 1435 1440

Asp Gly His Phe Glu Ile Leu Gly Lys Ile Ser Asn Val Ser Lys Asn 1445 1450 1455

Ala Lys Val Tyr Tyr Gly Asn Asn Tyr Lys Ser Ile Glu Ile Lys Ala 1460 1465 1470

Thr Lys Tyr Asp Phe His Ser Lys Thr Met Thr Phe Asp Leu Tyr Ala 1475 1480 1485

Asn Ile Asn Asp Ile Val Asp Gly Leu Ala Phe Ala Gly Asp Met Arg 1490 1495 1500

Leu Phe Val Lys Asp Asn Asp Gln Lys Lys Ala Glu Ile Lys Ile Arg 1505 1510 1515 1520

Met Pro Glu Lys Ile Lys Glu Thr Lys Ser Glu Tyr Pro Tyr Val Ser 1525 1530 1535

Ser Tyr Gly Asn Val Ile Glu Leu Gly Glu Gly Asp Leu Ser Lys Asn 1540 1545 1550

Lys Pro Asp Asn Leu Thr Lys Met Glu Ser Gly Lys Ile Tyr Ser Asp 1555 1560 1565

Ser Glu Lys Gln Gln Tyr Leu Leu Lys Asp Asn Ile Ile Leu Arg Lys 1570 1580

Gly Tyr Ala Leu Lys Val Thr Thr Tyr Asn Pro Gly Lys Thr Asp Met 1585 1590 1595 1600

Leu Glu Gly Asn Gly Val Tyr Ser Lys Glu Asp Ile Ala Lys Ile Gln
1605 1610 1615

Lys Ala Asn Pro Asn Leu Arg Ala Leu Ser Glu Thr Thr Ile Tyr Ala

Asp Ser Arg Asn Val Glu Asp Gly Arg Ser Thr Gln Ser Val Leu Met

Ser Ala Leu Asp Gly Phe Asn Ile Ile Arg Tyr Gln Val Phe Thr Phe

Lys Met Asn Asp Lys Gly Glu Ala Ile Asp Lys Asp Gly Asn Leu Val

Thr Asp Ser Ser Lys Leu Val Leu Phe Gly Lys Asp Asp Lys Glu Tyr

Thr Gly Glu Asp Lys Phe Asn Val Glu Ala Ile Lys Glu Asp Gly Ser

Met Leu Phe Ile Asp Thr Lys Pro Val Asn Leu Ser Met Asp Lys Asn

Tyr Phe Asn Pro Ser Lys Ser Asn Lys Ile Tyr Val Arg Asn Pro Glu

Phe Tyr Leu Arg Gly Lys Ile Ser Asp Lys Gly Gly Phe Asn Trp Glu

Leu Arg Val Asn Glu Ser Val Val Asp Asn Tyr Leu Ile Tyr Gly Asp

Leu His Ile Asp Asn Thr Arg Asp Phe Asn Ile Lys Leu Asn Val Lys

Asp Gly Asp Ile Met Asp Trp Gly Met Lys Asp Tyr Lys Ala Asn Gly

Phe Pro Asp Lys Val Thr Asp Met Asp Gly Asn Val Tyr Leu Gln Thr

Gly Tyr Ser Asp Leu Asn Ala Lys Ala Val Gly Val His Tyr Gln Phe

Leu Tyr Asp Asn Val Lys Pro Glu Val Asn Ile Asp Pro Lys Gly Asn

Thr Ser Ile Glu Tyr Ala Asp Gly Lys Ser Val Val Phe Asn Ile Asn

Asp Lys Arg Asn Asn Gly Phe Asp Gly Glu Ile Gln Glu Gln His Ile

Tyr Ile Asn Gly Lys Glu Tyr Thr Ser Phe Asn Asp Ile Lys Gln Ile

Ile Asp Lys Thr Leu Asn Ile Lys Ile Val Val Lys Asp Phe Ala Arg

Asn Thr Thr Val Lys Glu Phe Ile Leu Asn Lys Asp Thr Gly Glu Val

1925 1930 1935

Ser Glu Leu Lys Pro His Arg Val Thr Val Thr Ile Gln Asn Gly Lys 1940 1945 1950

Glu Met Ser Ser Thr Ile Val Ser Glu Glu Asp Phe Ile Leu Pro Val

Tyr Lys Gly Glu Leu Glu Lys Gly Tyr Gln Phe Asp Gly Trp Glu Ile 1970 1975 1980

Ser Gly Phe Glu Gly Lys Lys Asp Ala Gly Tyr Val Ile Asn Leu Ser 1985 1990 1995 2000

Lys Asp Thr Phe Ile Lys Pro Val Phe Lys Lys Ile Glu Glu Lys Lys 2005 2010 2015

Glu Glu Glu Asn Lys Pro Thr Phe Asp Val Ser Lys Lys Lys Asp Asn 2020 2025 2030

Pro Gln Val Asn His Ser Gln Leu Asn Glu Ser His Arg Lys Glu Asp 2035 2040 2045

Leu Gln Arg Glu Glu His Ser Gln Lys Ser Asp Ser Thr Lys Asp Val 2050 2055 2060

Thr Ala Thr Val Leu Asp Lys Asn Asn Ile Ser Ser Lys Ser Thr Thr 2065 2070 2075 2080

Asn Asn Pro Asn Lys Leu Pro Lys Thr Gly Thr Ala Ser Gly Ala Gln 2085 2090 2095

Thr Leu Leu Ala Ala Gly Ile Met Phe Ile Val Gly Ile Phe Leu Gly 2100 2105 2110

Leu Lys Lys Asn Gln Asp 2115

<210> 29

<211> 597

<212> DNA

<213> Streptococcus pneumoniae

<400> 29

cttgaattaa ataaaaaacg tcatgcgact aagcatttta ctgataagct tgttgatccc 60 aaagatgtgc gtacggctat cgaaattgca accttagcgc caagcgccca caacagccag 120 ccttggaaat ttgtggtgt acgtgagaaa aatgctgaac tggcaaagtt agcttatggt 180 tccaattttg aacaggtatc atcagcgcct gtaaccattg ccttgtttac agatacggac 240 ttagccaaac gtgctcgtaa gattgcccgt gttggtggtg ctaataactt ttctgaagag 300 caacttcaat atttatgaa aaatctgcca gctgagtttg cccgttacag tgagcaacaa 360 gtcagcgact acctagctc caatgcaggt ttggttgcca tgaacttggt tcttgcattg 420 acagaccaag gaattggtc taacattatt cttggttttg acaaatcaaa agttaatgaa 480 gttttggaaa tcgaagacc tttccgccca gaactcttga tcacagtggg ttaacagac 540 gaaaaaattgg aaccaagcta ccgcttgcca gtagatgaaa tcatcgagaa aagatag 597

<210> 30

<211> 198

<212> PRT

<213> Streptococcus pneumoniae

<400> 30

Leu Glu Leu Asn Lys Lys Arg His Ala Thr Lys His Phe Thr Asp Lys

1 5 10 15

Leu Val Asp Pro Lys Asp Val Arg Thr Ala Ile Glu Ile Ala Thr Leu 20 25 30

Ala Pro Ser Ala His Asn Ser Gln Pro Trp Lys Phe Val Val Arg 35 40 45

Glu Lys Asn Ala Glu Leu Ala Lys Leu Ala Tyr Gly Ser Asn Phe Glu 50 55 60

Gln Val Ser Ser Ala Pro Val Thr Ile Ala Leu Phe Thr Asp Thr Asp 65 70 75 80

Leu Ala Lys Arg Ala Arg Lys Ile Ala Arg Val Gly Gly Ala Asn Asn 85 90 95

Phe Ser Glu Glu Gln Leu Gln Tyr Phe Met Lys Asn Leu Pro Ala Glu 100 105 110

Phe Ala Arg Tyr Ser Glu Gln Gln Val Ser Asp Tyr Leu Ala Leu Asn 115 120 125

Ala Gly Leu Val Ala Met Asn Leu Val Leu Ala Leu Thr Asp Gln Gly 130 135 140

Ile Gly Ser Asn Ile Ile Leu Gly Phe Asp Lys Ser Lys Val Asn Glu 145 150 155 160

Val Leu Glu Ile Glu Asp Arg Phe Arg Pro Glu Leu Leu Ile Thr Val 165 170 175

Gly Tyr Thr Asp Glu Lys Leu Glu Pro Ser Tyr Arg Leu Pro Val Asp 180 185 190

Glu Ile Ile Glu Lys Arg 195

<210> 31

<211> 1401

<212> DNA

<213> Streptococcus pneumoniae

<400> 31

atgacagcaa ttgattttac agcagaagta gaaaaacgca aagaagacct cttggctgac 60 ttgtttagcc ttttggaaat caattcagaa cgtgatgaca gcaaggctga tgcccagcat 120 ccatttgggc ctggtccagt aaaagccttg gagaaattcc ttgaaatcgc agaccgcgat 180

ggctacccaa ctaagaatgt tgataactat gcaggacatt ttgagtttgg tgatggagaa 240 gaagtteteg gaatetttge eeatatggat gtggtgeetg etggtagegg ttgggacaca 300 qaccettaca caccaactat caaagatggt cgcetttatg cgcgcggggc ttcggacgat 360 aagggtccta caacagcttg ttactatggt ttgaaaatca tcaaagaatt gggtcttcca 420 acttctaaga aagttcgctt catcgttgga acagacgaag aatcaggctg ggcagacatg 480 gactactact ttgagcacgt aggacttgcc aaaccagatt tcggtttctc accagatgct 540 gaatttccaa tcatcaatgg tgaaaaagga aatatcacgg aatacctcca ctttgcagga 600 qaaaatacag gtgttgcccg tcttcacagc tttacaggtg gtttacgtga aaatatggta 660 ccagaatcag caacagcagt cgtttcaggt gacttggctg acttgcaagc taaactagat 720 qcctttgttg cagaacacaa acttagagga gaactccaag aagaagctgg caaatacaag 780 gtgacgatca ttggtaaatc agcccacggt gctatgcctg cttcaggtgt caatggcgca 840 acttaccttg ccctcttcct cagccagttt ggctttgctg gtccagccaa agactacctt 900 gacatcgcag gtaaaattct cttgaacgat catgagggtg aaaatcttaa gattgctcat 960 gtggatgaaa agatgggtgc tctttctatg aatgccggcg tcttccactt cgatgaaaca 1020 agtgctgata ataccattgc cctcaacatc cgctatccaa aaggaacaag tccagaacaa 1080 atcaagtcaa toottgaaaa ottgocagtt gtttotgtta gootgtotga acacggtcac 1140 acgcctcact atgtgccaat ggaagatcca cttgtgcaaa ccttgttgaa tatctatgaa 1200 aaacaaactg gctttaaagg tcatgaacaa gtcatcggtg gtggaacctt tggtcgcttg 1260 ctagaacgcg gagttgccta cggtgctatg ttcccagact cgattgatac catgcaccaa 1320 gccaatgaat ttatcgcctt ggatgatctt ttccgagcag cagcaattta tgccgaagct 1380 1401 atttacgaat tgatcaaata a

<210> 32

<211> 466

<212> PRT

<213> Streptococcus pneumoniae

<400> 32

Met Thr Ala Ile Asp Phe Thr Ala Glu Val Glu Lys Arg Lys Glu Asp

Leu Leu Ala Asp Leu Phe Ser Leu Leu Glu Ile Asn Ser Glu Arg Asp 20 25 30

Asp Ser Lys Ala Asp Ala Gln His Pro Phe Gly Pro Gly Pro Val Lys
35 40 45

Ala Leu Glu Lys Phe Leu Glu Ile Ala Asp Arg Asp Gly Tyr Pro Thr 50 55 60

Lys Asn Val Asp Asn Tyr Ala Gly His Phe Glu Phe Gly Asp Gly Glu 65 70 75 80

Glu Val Leu Gly Ile Phe Ala His Met Asp Val Val Pro Ala Gly Ser 85 90 95

Gly Trp Asp Thr Asp Pro Tyr Thr Pro Thr Ile Lys Asp Gly Arg Leu 100 105 110

Tyr Ala Arg Gly Ala Ser Asp Asp Lys Gly Pro Thr Thr Ala Cys Tyr 115 120 125

Tyr Gly Leu Lys Ile Ile Lys Glu Leu Gly Leu Pro Thr Ser Lys Lys 130 135 140

Val Arg Phe Ile Val Gly Thr Asp Glu Glu Ser Gly Trp Ala Asp Met

145 150 155 160

Asp Tyr Tyr Phe Glu His Val Gly Leu Ala Lys Pro Asp Phe Gly Phe 165 170 175

Ser Pro Asp Ala Glu Phe Pro Ile Ile Asn Gly Glu Lys Gly Asn Ile 180 185 190

Thr Glu Tyr Leu His Phe Ala Gly Glu Asn Thr Gly Val Ala Arg Leu 195 200 205

His Ser Phe Thr Gly Gly Leu Arg Glu Asn Met Val Pro Glu Ser Ala 210 215 220

Thr Ala Val Val Ser Gly Asp Leu Ala Asp Leu Gln Ala Lys Leu Asp 225 230 235 240

Ala Phe Val Ala Glu His Lys Leu Arg Gly Glu Leu Gln Glu Glu Ala 245 250 255

Gly Lys Tyr Lys Val Thr Ile Ile Gly Lys Ser Ala His Gly Ala Met 260 265 270

Pro Ala Ser Gly Val Asn Gly Ala Thr Tyr Leu Ala Leu Phe Leu Ser 275 280 285

Gln Phe Gly Phe Ala Gly Pro Ala Lys Asp Tyr Leu Asp Ile Ala Gly 290 295 300

Lys Ile Leu Leu Asn Asp His Glu Gly Glu Asn Leu Lys Ile Ala His 305 310 315 320

Val Asp Glu Lys Met Gly Ala Leu Ser Met Asn Ala Gly Val Phe His 325 330 335

Phe Asp Glu Thr Ser Ala Asp Asn Thr Ile Ala Leu Asn Ile Arg Tyr 340 345 350

Pro Lys Gly Thr Ser Pro Glu Gln Ile Lys Ser Ile Leu Glu Asn Leu 355 360 365

Pro Val Val Ser Val Ser Leu Ser Glu His Gly His Thr Pro His Tyr 370 375 380

Val Pro Met Glu Asp Pro Leu Val Gln Thr Leu Leu Asn Ile Tyr Glu 385 390 395 400

Lys Gln Thr Gly Phe Lys Gly His Glu Gln Val Ile Gly Gly Thr 405 410 415

Phe Gly Arg Leu Leu Glu Arg Gly Val Ala Tyr Gly Ala Met Phe Pro 420 425 430

Asp Ser Ile Asp Thr Met His Gln Ala Asn Glu Phe Ile Ala Leu Asp 435 440 445

Asp Leu Phe Arg Ala Ala Ala Ile Tyr Ala Glu Ala Ile Tyr Glu Leu

460 455 450

Ile Lys 465

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<400> 33 gtgtatacta ttataaaatc aaatataaaa aaatttagtt tattaacgat atttattgtt 60 gctggtcaat tattgctaat ttatgcagca actattaatg ctctggtgtt gaatgaatta 120 attgcgatga atttagagcg gtttttgaaa ttgtcaatct accaaatgat tgtctggtgt 180 gggataatat tccttgactg ggtagtgaaa aattatcagg ttgaagtgat ccaagagttt 240 aatctagaga ttcgaaatag agttgccaca gacatctcta actctaccta tcaagaattt 300 catagtaaat catcaggaac atatctttcg tggctaaata atgatgttca gactttaaat 360 gatcaggcgt ttaaacaact ttttttagta ataaaaggaa tttctggtac tatatttgca 420 gttgtgactc ttaatcacta tcattggtca ttgactgtag ccaccttgtt ttcattaatg 480 attatgctac ttgtaccaaa aatctttgca tcgaaaatgc gagaagttag tctaaattta 540 actaaccaaa atgaagcttt tttaaaatct agtgagacta tattgaatgg atttgatgtg 600 ttagcgtcct tgaatctttt atatgtattg cctaagaaaa ttaaagaagc aggaatttta 660 ttaaaqatgq ttatacaaag aaagacaact gtagaaacgt tagcaggcgc tattagcttc 720 tttctcaata tttttttca gatatctctc gtttttttaa caggctatct tgcaataaaa 780 ggaatagtga aaattggtac tattgaagca ataggagcac taacaggtgt tatttttaca 840 gcgctaggtg aattaggagg tcaattatcc tctattattg gtacgaagcc tatttttta 900 aaattgtatt caattaatcc aattgagtca aataaaatga atgatatcga accaaatgag 960 gtgaatagag attttccgtt atatgaagca aaaaatattt gctataagta tggagataaa 1020 gaaatattaa aaaacttaaa tttttgtttt caacgtaatg aaaagtattt aattttaggt 1080 gaaagtggaa gcgggaaatc tacattatta aaattattga atggcttttt gagagattat 1140 agtggagaat tgcgattctg cggggatgat ataaaaaaaa cctcctattt aaatatggtt 1200 tcgaatgttc tatatgtaga tcaaaaagct tatttgtttg aaggtacgat tagagataat 1260 attttattgg aagaaaatta tactgatgaa gaaatactac agtctttaga gcaagttggt 1320 ttgagtgtaa aagattttcc taataacatt ttagattatt atgttggtga tgatgggaga 1380 ttactgtcag gagggcagaa acaaaaaatt actttagcta gagggctaat tagaaataag 1440 aaaatagtat taattgacga gggaacttct gctatcgata ggagaacttc gttagcgatt 1500 gaacgtaaga tattagatag agaggatttg actgtcatta ttgttaccca tgctccgcat 1560 ceggaactta aacaatattt tactaagata tatcaatttc caaaggattt tatttaa

<210> 34 <211> 538

<212> PRT

<213> Streptococcus pneumoniae

<400> 34

Met Tyr Thr Ile Ile Lys Ser Asn Ile Lys Lys Phe Ser Leu Leu Thr 1

Ile Phe Ile Val Ala Gly Gln Leu Leu Leu Ile Tyr Ala Ala Thr Ile 25

Asn Ala Leu Val Leu Asn Glu Leu Ile Ala Met Asn Leu Glu Arg Phe 45 40 35

- Leu Lys Leu Ser Ile Tyr Gln Met Ile Val Trp Cys Gly Ile Ile Phe 50 55 60
- Leu Asp Trp Val Val Lys Asn Tyr Gln Val Glu Val Ile Gln Glu Phe 65 70 75 80
- Asn Leu Glu Ile Arg Asn Arg Val Ala Thr Asp Ile Ser Asn Ser Thr 85 90 95
- Tyr Gln Glu Phe His Ser Lys Ser Ser Gly Thr Tyr Leu Ser Trp Leu 100 105 110
- Asn Asn Asp Val Gln Thr Leu Asn Asp Gln Ala Phe Lys Gln Leu Phe 115 120 125
- Leu Val Ile Lys Gly Ile Ser Gly Thr Ile Phe Ala Val Val Thr Leu 130 135 140
- Asn His Tyr His Trp Ser Leu Thr Val Ala Thr Leu Phe Ser Leu Met 145 150 155 160
- Ile Met Leu Leu Val Pro Lys Ile Phe Ala Ser Lys Met Arg Glu Val 165 170 175
- Ser Leu Asn Leu Thr Asn Gln Asn Glu Ala Phe Leu Lys Ser Ser Glu 180 185 190
- Thr Ile Leu Asn Gly Phe Asp Val Leu Ala Ser Leu Asn Leu Leu Tyr 195 200 205
- Val Leu Pro Lys Lys Ile Lys Glu Ala Gly Ile Leu Leu Lys Met Val 210 215 220
- Ile Gln Arg Lys Thr Thr Val Glu Thr Leu Ala Gly Ala Ile Ser Phe 225 230 235 240
- Phe Leu Asn Ile Phe Phe Gln Ile Ser Leu Val Phe Leu Thr Gly Tyr 245 250 255
- Leu Ala Ile Lys Gly Ile Val Lys Ile Gly Thr Ile Glu Ala Ile Gly 260 265 270
- Ala Leu Thr Gly Val Ile Phe Thr Ala Leu Gly Glu Leu Gly Gln 275 280 285
- Leu Ser Ser Ile Ile Gly Thr Lys Pro Ile Phe Leu Lys Leu Tyr Ser 290 295 300
- Ile Asn Pro Ile Glu Ser Asn Lys Met Asn Asp Ile Glu Pro Asn Glu 305 310 315 320
- Val Asn Arg Asp Phe Pro Leu Tyr Glu Ala Lys Asn Ile Cys Tyr Lys 325 330 335
- Tyr Gly Asp Lys Glu Ile Leu Lys Asn Leu Asn Phe Cys Phe Gln Arg 340 345 350

Asn Glu Lys Tyr Leu Ile Leu Gly Glu Ser Gly Ser Gly Lys Ser Thr 360 355 Leu Leu Lys Leu Leu Asn Gly Phe Leu Arg Asp Tyr Ser Gly Glu Leu 375 Arg Phe Cys Gly Asp Asp Ile Lys Lys Thr Ser Tyr Leu Asn Met Val 395 390 Ser Asn Val Leu Tyr Val Asp Gln Lys Ala Tyr Leu Phe Glu Gly Thr 410 405 Ile Arg Asp Asn Ile Leu Leu Glu Glu Asn Tyr Thr Asp Glu Glu Ile 425 Leu Gln Ser Leu Glu Gln Val Gly Leu Ser Val Lys Asp Phe Pro Asn 435 Asn Ile Leu Asp Tyr Tyr Val Gly Asp Asp Gly Arg Leu Leu Ser Gly Gly Gln Lys Gln Lys Ile Thr Leu Ala Arg Gly Leu Ile Arg Asn Lys 475 470 Lys Ile Val Leu Ile Asp Glu Gly Thr Ser Ala Ile Asp Arg Arg Thr 490 485 Ser Leu Ala Ile Glu Arg Lys Ile Leu Asp Arg Glu Asp Leu Thr Val 505 Ile Ile Val Thr His Ala Pro His Pro Glu Leu Lys Gln Tyr Phe Thr 525 515 520 Lys Ile Tyr Gln Phe Pro Lys Asp Phe Ile 535 530 <210> 35 <211> 705 <212> DNA <213> Streptococcus pneumoniae <400> 35 ataacagtta aacagattat ggacgaaata gccgtttcag atatgactgc aaggcgctat 60 ttacaggaat tagctgataa agatttgctg attcgtgtgc atggtggagc tgaaaaactt 120 cgaaccaact cccttttgac taatgagcga tcaaatattg aaaaacaagc cctccaaacg 180 gcagaaaaac aagaaatagc ccattttgca ggcagtctag tagaagaaag agaaactatt 240 ttcattggac caggaacaac attagagttt tttgcgcgtg agttgcctat tgacaatatc 300 cgcgtcgtaa ccaacagtct acctgttttt ctgattttaa gcgaacgaaa attaacagat 360 ttgattttaa taggtggaaa ttatcgcgat attacaggtg cttttgttgg tacattgacc 420 ctacaaaatc tctctaatct ccaattttct aaagctttcg ttagctgtaa tggtattcaa 480 aacggagctc tagctacttt tagcgaggaa gagggagagg ctcaacgcat cgctttaaat 540 aattctaata aaaaatattt actcgcagat catagcaagt tcaataagtt tgatttttat 600 actttttata atgtatcaaa tottgatact attgtttcag attctaaact aagtgattca 660

atccttttta agctatctaa acacattaaa gtcatcaagc cttaa

705

<210> 36

<211> 234

<212> PRT

<213> Streptococcus pneumoniae

<400> 36

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Ala Arg Arg Tyr Leu Gln Glu Leu Ala Asp Lys Asp Leu Leu Ile Arg 20 25 30

Val His Gly Gly Ala Glu Lys Leu Arg Thr Asn Ser Leu Leu Thr Asn 35 40 45

Glu Arg Ser Asn Ile Glu Lys Gln Ala Leu Gln Thr Ala Glu Lys Gln
50 55 60

Glu Ile Ala His Phe Ala Gly Ser Leu Val Glu Glu Arg Glu Thr Ile
65 70 75 80

Phe Ile Gly Pro Gly Thr Thr Leu Glu Phe Phe Ala Arg Glu Leu Pro

Ile Asp Asn Ile Arg Val Val Thr Asn Ser Leu Pro Val Phe Leu Ile 100 105 110

Leu Ser Glu Arg Lys Leu Thr Asp Leu Ile Leu Ile Gly Gly Asn Tyr 115 120 125

Arg Asp Ile Thr Gly Ala Phe Val Gly Thr Leu Thr Leu Gln Asn Leu 130 135 140

Ser Asn Leu Gln Phe Ser Lys Ala Phe Val Ser Cys Asn Gly Ile Gln 145 150 155 160

Asn Gly Ala Leu Ala Thr Phe Ser Glu Glu Glu Glu Glu Ala Gln Arg 165 170 175

Ile Ala Leu Asn Asn Ser Asn Lys Lys Tyr Leu Leu Ala Asp His Ser 180 185 190

Lys Phe Asn Lys Phe Asp Phe Tyr Thr Phe Tyr Asn Val Ser Asn Leu 195 200 205

Asp Thr Ile Val Ser Asp Ser Lys Leu Ser Asp Ser Ile Leu Phe Lys 210 215 220

Leu Ser Lys His Ile Lys Val Ile Lys Pro 225 230

<210> 37

<211> 483

<212> DNA

<213> Streptococcus pneumoniae

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Gln Asp Ile Thr Ile Val Val Glu Leu Met Gly Arg Ile Glu Pro Ala 65 70 75 80

Lys Thr Phe Ile Thr Arg Ala Leu Glu Ala Gly Lys His Val Val Thr 85 90 95

Ala Asn Lys Asp Leu Leu Ala Val His Gly Ala Glu Leu Leu Glu Ile 100 105 110

Ala Gln Ala Asn Lys Val Ala Leu Tyr Tyr Glu Ala Ala Val Ala Gly 115 120 125 Gly Ile Pro Ile Leu Arg Thr Leu Ala Asn Ser Leu Ala Ser Asp Lys

Ile Thr Arg Val Leu Gly Val Val Asn Gly Thr Ser Asn Phe Met Val 155

Thr Lys Met Val Glu Glu Gly Trp Ser Tyr Asp Asp Ala Leu Ala Glu 170

Ala Gln Arg Leu Gly Phe Ala Glu Ser Asp Pro Thr Asn Asp Val Asp 185

Gly Ile Asp Ala Ala Tyr Lys Met Val Ile Leu Ser Gln Phe Ala Phe 200

Gly Met Lys Ile Ala Phe Asp Asp Val Ala His Lys Gly Ile Arg Asn 215

Ile Thr Pro Glu Asp Val Ala Val Ala Gln Glu Leu Gly Tyr Val Val 235 230

Lys Leu Val Gly Ser Ile Glu Glu Thr Ser Ser Gly Ile Ala Ala Glu 245

Val Thr Pro Thr Phe Leu Pro Lys Ala His Pro Leu Ala Ser Val Asn 265

Gly Val Met Asn Ala Val Phe Val Glu Ser Ile Gly Ile Gly Glu Ser 275

Met Tyr Tyr Gly Pro Gly Ala Gly Gln Lys Pro Thr Ala Thr Ser Val

Val Ala Asp Ile Val Arg Ile Val Arg Arg Leu Asn Asp Gly Thr Ile 310

Gly Lys Asp Phe Asn Glu Tyr Ser Arg Asp Leu Val Leu Ala Asn Pro 325

Glu Asp Val Lys Ala Asn Tyr Tyr Phe Ser Ile Leu Ala Leu Asp Ser 345

Lys Gly Gln Val Leu Lys Leu Ala Glu Ile Phe Asn Ala Gln Asp Ile 355

Ser Phe Lys Gln Ile Leu Gln Asp Gly Lys Glu Gly Asp Lys Ala Arg 375

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- Ala Val Gly Ser Ala Lys Glu Leu Thr Asn Asp Leu Tyr Arg His Ile 85 90 95
- Leu Ser Leu Pro Lys Asp Ser Arg Asp Arg Leu Thr Thr Ser Ser Leu 100 105 110
- Val Thr Arg Leu Thr Ser Asp Thr Tyr Gln Ile Gln Thr Gly Ile Asn 115 120 125
- Gln Phe Leu Arg Leu Phe Leu Arg Ala Pro Ile Ile Val Phe Gly Ala 130 135 140
- Val Leu Val Ala Ile Leu Thr Ile Val Ile Val Gly Leu Ser Arg Leu
 165 170 175
- Val Asn Pro Phe Tyr Ser Ser Leu Arg Lys Lys Thr Asp Gln Leu Val
- Gln Glu Thr Arg Gln Gln Leu Gln Gly Met Arg Val Ile Arg Ala Phe 195 200 205
- Gly Gln Glu Lys Arg Glu Leu Gln Ile Phe Gln Thr Leu Asn Gln Val 210 215 220
- Tyr Ala Arg Leu Gln Glu Lys Thr Gly Phe Trp Ser Ser Leu Leu Thr 225 230 235 240
- Pro Leu Thr Tyr Leu Ile Val Asn Gly Thr Leu Leu Val Ile Ile Trp 245 250 255
- Gln Gly Tyr Ile Ser Ile Gln Gly Gly Val Leu Ser Gln Gly Ala Leu 260 265 270
- Ile Ala Leu Ile Asn Tyr Leu Leu Gln Ile Leu Val Glu Leu Val Lys 275 280 285
- Leu Ala Met Leu Ile Asn Ser Leu Asn Gln Ser Tyr Ile Ser Val Lys 290 295 300
- Arg Ile Glu Glu Val Phe Val Glu Ala Pro Glu Asp Ile His Ser Glu 305 310 315 320
- Leu Glu Gln Lys Gln Ala Thr Arg Asp Lys Val Leu Gln Val Gln Glu 325 330 335
- Leu Thr Phe Thr Tyr Pro Asp Ala Ala Gln Pro Ser Leu Arg Tyr Ile 340 345 350
- Ser Phe Asp Met Thr Gln Gly Gln Ile Leu Gly Ile Ile Gly Gly Thr 355 360 365

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Ala Ser Thr Gly Ala Lys Asn Trp Val Ser Ile Asn Gly Ile Thr Leu 100 105 110

Phe Gln Pro Ser Glu Phe Met Lys Ile Ser Tyr Ile Leu Met Leu Ala 115 120 125

Arg Val Ile Val Gln Phe Thr Lys Lys His Lys Glu Trp Arg Arg Thr 130 135 140

Val Pro Leu Asp Phe Leu Leu Ile Phe Trp Met Ile Leu Phe Thr Ile 145 150 155 160

Pro Val Leu Val Leu Leu Ala Leu Gln Ser Asp Leu Gly Thr Ala Leu 165 170 175

Val Phe Val Ala Ile Phe Ser Gly Ile Val Leu Leu Ser Gly Val Ser

Trp Lys Ile Ile Pro Val Phe Val Thr Ala Val Thr Gly Val Ala

205 200

195 Gly Phe Leu Ala Ile Phe Ile Ser Lys Asp Gly Arg Ala Phe Leu His 215 210 Gln Ile Gly Met Pro Thr Tyr Gln Ile Asn Arg Ile Leu Ala Trp Leu 235 Asn Pro Phe Glu Phe Ala Gln Thr Thr Thr Tyr Gln Gln Ala Gln Gly 250 245 Gln Ile Ala Ile Gly Ser Gly Gly Leu Phe Gly Gln Gly Phe Asn Ala 265 260 Ser Asn Leu Leu Ile Pro Val Arg Glu Ser Asp Met Ile Phe Thr Val 280 Ile Ala Glu Asp Phe Gly Phe Ile Gly Ser Val Leu Val Ile Ala Leu 295 Tyr Leu Met Leu Ile Tyr Arg Met Leu Lys Ile Thr Leu Lys Ser Asn 315 305 310 Asn Gln Phe Tyr Thr Tyr Ile Ser Thr Gly Leu Ile Met Met Leu Leu 330 325 Phe His Ile Phe Glu Asn Ile Gly Ala Val Thr Gly Leu Leu Pro Leu 350 340 Thr Gly Ile Pro Leu Pro Phe Ile Ser Gln Gly Gly Ser Ala Ile Ile Ser Asn Leu Ile Gly Val Gly Leu Leu Leu Ser Met Ser Tyr Gln Thr 370 375 Asn Leu Ala Glu Glu Lys Ser Gly Lys Val Pro Phe Lys Arg Lys Lys 400 395 385 390 Val Val Leu Lys Gln Ile Lys 405

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200

Glu Asn Lys Gly Ser Asp Arg Val Val Glu Val Ile Arg Leu Leu His 215 Gln Glu Gly Lys Asn Tyr His Leu Tyr Phe Ile Gly Ala Gly Asp Met 240 235 230 Glu Glu Glu Leu Lys Lys Arg Val Lys Glu Tyr Gly Ile Glu Asp Tyr Val His Phe Leu Gly Tyr Gln Lys Asn Pro Tyr Gln Tyr Leu Ser Gln 265 Thr Lys Val Leu Leu Ser Met Ser Lys Gln Glu Gly Phe Pro Gly Val 275 280 Tyr Val Glu Ala Leu Ser Leu Gly Leu Pro Phe Ile Ser Thr Asp Val 295 Gly Gly Ala Glu Glu Leu Ser Gln Glu Gly Arg Phe Gly Gln Ile Ile 315 310 Glu Ser Asn Gln Glu Ala Ala Gln Ala Ile Thr Asn Tyr Met Thr Ser 325 Ala Ser Asn Phe Asp Val Asp Glu Ala Ser Gln Phe Ile Gln Gln Phe 345 Thr Ile Thr Lys Gln Ile Glu Gln Val Glu Lys Leu Leu Glu Glu 355 360 <210> 47 <211> 987 <212> DNA <213> Streptococcus pneumoniae <400> 47 atggaaactg cattaattag tgtgattgtg ccagtctata atgtggcgca gtacctagaa 60 aaatcgatag cttccattca gaagcagacc tatcaaaatc tggaaattat tcttgttgat 120 gatggtgcaa cagatgaaag tggtcgcttg tgtgattcaa tcgctgaaca agatgacagg 180 gtgtcagtgc ttcataaaaa gaacgaagga ttgtcgcaag cacgaaatga tgggatgaag 240 caggeteacg gggattatet gatttttatt gacteagatg attatateca tecagaaatg 300 attcagaget tatatgagea attagtteaa gaagatgegg atgtttegag etgtggtgte 360 atgaatgtct atgctaatga tgaaagccca cagtcagcca atcaggatga ctattttgtc 420 tgtgattctc aaacatttct aaaggaatac ctcataggtg aaaaaatacc tgggacgatt 480 tqcaataagc taatcaagag acagattgca actgccctat cctttcctaa ggggttgatt 540 tacgaagatg cctattacca ttttgattta atcaagttgg ccaagaagta tgtggttaat 600 actaaaccct attattacta tttccataga ggggatagta ttacgaccaa accctatgca 660 qaqaaqqatt tagcctatat tgatatctac caaaagtttt ataatgaagt tgtgaaaaac 720 tatcctgact tgaaagaggt cgcttttttc agattggcct atgcccactt ctttattctg 780 gataagatgt tgctagatga tcagtataaa cagtttgaag cctattctca gattcatcgt 840

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Asn Leu Glu Ile Ile Leu Val Asp Asp Gly Ala Thr Asp Glu Ser Gly 35 40 45

Arg Leu Cys Asp Ser Ile Ala Glu Gln Asp Asp Arg Val Ser Val Leu
50 55 60

His Lys Lys Asn Glu Gly Leu Ser Gln Ala Arg Asn Asp Gly Met Lys 65 70 75 80

Gln Ala His Gly Asp Tyr Leu Ile Phe Ile Asp Ser Asp Asp Tyr Ile 85 90 95

His Pro Glu Met Ile Gln Ser Leu Tyr Glu Gln Leu Val Gln Glu Asp 100 105 110

Ala Asp Val Ser Ser Cys Gly Val Met Asn Val Tyr Ala Asn Asp Glu 115 120 125

Ser Pro Gln Ser Ala Asn Gln Asp Asp Tyr Phe Val Cys Asp Ser Gln 130 135 140

Thr Phe Leu Lys Glu Tyr Leu Ile Gly Glu Lys Ile Pro Gly Thr Ile 145 150 155 160

Cys Asn Lys Leu Ile Lys Arg Gln Ile Ala Thr Ala Leu Ser Phe Pro 165 170 175

Lys Gly Leu Ile Tyr Glu Asp Ala Tyr Tyr His Phe Asp Leu Ile Lys 180 $$ 185 $$ 190 $$

Leu Ala Lys Lys Tyr Val Val Asn Thr Lys Pro Tyr Tyr Tyr Tyr Phe 195 200 205

His Arg Gly Asp Ser Ile Thr Thr Lys Pro Tyr Ala Glu Lys Asp Leu 210 215 220

Ala Tyr Ile Asp Ile Tyr Gln Lys Phe Tyr Asn Glu Val Val Lys Asn 225 230 235 240

Tyr Pro Asp Leu Lys Glu Val Ala Phe Phe Arg Leu Ala Tyr Ala His 245 250 255

Phe Phe Ile Leu Asp Lys Met Leu Leu Asp Asp Gln Tyr Lys Gln Phe 260 265 270

Glu Ala Tyr Ser Gln Ile His Arg Phe Leu Lys Gly His Ala Phe Ala 280 Ile Ser Arg Asn Pro Ile Phe Arg Lys Gly Arg Arg Ile Ser Ala Leu 295 290 Ala Leu Phe Ile Asn Ile Ser Leu Tyr Arg Phe Leu Leu Lys Asn 315 310 305 Ile Glu Lys Ser Lys Lys Leu His 325 <210> 49 <211> 735 <212> DNA <213> Streptococcus pneumoniae <400> 49 atgagaatca aagagaaaac caataatatt aatggaggaa taaaaaatgt aagtaagcat 60 tatggtcatt caatcattct caaagatata aattttgcac ttaacaaggg tgaaattgtt 120 ggtctagcag ggagaaatgg agttggtaag agtacgttga tgaaaattct tgttcagaat 180 aatcaaccga cttcaggtaa tattataagc agtgataatg ttgggtattt aatcgaagaa 240 ccaaaattat ttttatctaa aacaggttta gagaatttaa aatatttgtc aaatttatat 300 ggtgttgact acaatcaaga aagatttaga tgtttgatcc aagagttaga tttgactcag 360 tctattaata aaaaagtaaa gacctattct ttgggtacaa aacaaaaatt agctttgctt 420 ctaactctcg ttacggaacc tgatatattg attttagatg aaccgactaa tggtttagat 480 attgaatcat cacaaatagt tttagcggtt ctaaaaaaat tagctttaca tgaaaatgtg 540 ggaattttaa tatcgagtca taaattagaa gacattgaag aaatttgtga gagagttctt 600 ttcttggaga acgggctttt gacatttcaa aaagtaggaa aagatagtca taatttcttg 660 tttgagatag ctttttcatc agctacagat agagacattt tcattaccaa acaagaattt 720 735 tgggatattg tttag <210> 50 <211> 244 <212> PRT <213> Streptococcus pneumoniae <400> 50 Met Arg Ile Lys Glu Lys Thr Asn Asn Ile Asn Gly Gly Ile Lys Asn Val Ser Lys His Tyr Gly His Ser Ile Ile Leu Lys Asp Ile Asn Phe 20 Ala Leu Asn Lys Gly Glu Ile Val Gly Leu Ala Gly Arg Asn Gly Val Gly Lys Ser Thr Leu Met Lys Ile Leu Val Gln Asn Asn Gln Pro Thr 55 Ser Gly Asn Ile Ile Ser Ser Asp Asn Val Gly Tyr Leu Ile Glu Glu

75

70

Pro Lys Leu Phe Leu Ser Lys Thr Gly Leu Glu Asn Leu Lys Tyr Leu 85 Ser Asn Leu Tyr Gly Val Asp Tyr Asn Gln Glu Arg Phe Arg Cys Leu 105 100 Ile Gln Glu Leu Asp Leu Thr Gln Ser Ile Asn Lys Lys Val Lys Thr 120 Tyr Ser Leu Gly Thr Lys Gln Lys Leu Ala Leu Leu Leu Thr Leu Val 135 Thr Glu Pro Asp Ile Leu Ile Leu Asp Glu Pro Thr Asn Gly Leu Asp 155 150 Ile Glu Ser Ser Gln Ile Val Leu Ala Val Leu Lys Lys Leu Ala Leu 165 His Glu Asn Val Gly Ile Leu Ile Ser Ser His Lys Leu Glu Asp Ile 185 180 Glu Glu Ile Cys Glu Arg Val Leu Phe Leu Glu Asn Gly Leu Leu Thr 205 200 Phe Gln Lys Val Gly Lys Asp Ser His Asn Phe Leu Phe Glu Ile Ala 210 215 Phe Ser Ser Ala Thr Asp Arg Asp Ile Phe Ile Thr Lys Gln Glu Phe 235 230 Trp Asp Ile Val <210> 51 <211> 1704 <212> DNA <213> Streptococcus pneumoniae <400> 51 atgactgaat tagataaacg tcaccgcagt agcatttatg acagcatggt taaatcacct 60 aaccgtgcta tgcttcgtgc gactggtatg acagataagg actttgaaac atcgattgtg 120 ggagtgattt cgacttgggc ggaaaataca ccatgtaaca ttcacttgca tgatttcggg 180 aaactggcta aagaaggtgt caaatctgca ggcgcttggc ctgtacagtt tggaaccatt 240 accgtagcgg acgggatcgc tatgggaacg cctggtatgc gtttctctct aacatctcgt 300 gacatcatcg cggactccat cgaggcggct atgagtggtc acaacgtgga tgccttcgtc 360 gctatcggtg gctgtgacaa gaacatgcct ggatctatga ttgctattgc taatatggat 420 atcccagcta ttttcgccta tggtggaact attgcaccgg gaaatcttga tggtaaagat 480 atcqacttgg tttctgtctt tgaaggtatc ggaaaatgga accacggtga catgacagct 540 qaqqacqtqa aacqtcttga atgtaatgcc tgccctggcc ctggtggttg tggtggtatg 600 tatactgcta ataccatggc aactgctatc gaagttctag ggatgagttt gccagggtca 660 tecteteace cagetgaate agetgataag aaagaagata tegaageage aggaegtget 720 gttgttaaga tgttggaact tggtctcaaa ccatcagata tcttgactcg tgaagccttt 780 gaagatgcta tcactgtaac gatggctctc ggtggttcta caaacgccac tcttcacttg 840

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<210> 52 <211> 567 <212> PRT <213> Streptococcus pneumoniae

Val Lys Ser Pro Asn Arg Ala Met Leu Arg Ala Thr Gly Met Thr Asp 20 25 30

Lys Asp Phe Glu Thr Ser Ile Val Gly Val Ile Ser Thr Trp Ala Glu 35 40 45

Asn Thr Pro Cys Asn Ile His Leu His Asp Phe Gly Lys Leu Ala Lys 50 55 60

Glu Gly Val Lys Ser Ala Gly Ala Trp Pro Val Gln Phe Gly Thr Ile 65 70 75 80

Thr Val Ala Asp Gly Ile Ala Met Gly Thr Pro Gly Met Arg Phe Ser 85 90 95

Leu Thr Ser Arg Asp Ile Ile Ala Asp Ser Ile Glu Ala Ala Met Ser 100 105 110

Gly His Asn Val Asp Ala Phe Val Ala Ile Gly Gly Cys Asp Lys Asn 115 120 125

Met Pro Gly Ser Met Ile Ala Ile Ala Asn Met Asp Ile Pro Ala Ile 130 135 140

Phe Ala Tyr Gly Gly Thr Ile Ala Pro Gly Asn Leu Asp Gly Lys Asp 145 150 155 160

Ile Asp Leu Val Ser Val Phe Glu Gly Ile Gly Lys Trp Asn His Gly 165 170 175

Asp Met Thr Ala Glu Asp Val Lys Arg Leu Glu Cys Asn Ala Cys Pro 180 185 190 Gly Pro Gly Gly Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala Thr
195 200 205

• • •

- Ala Ile Glu Val Leu Gly Met Ser Leu Pro Gly Ser Ser Ser His Pro 210 215 220
- Ala Glu Ser Ala Asp Lys Lys Glu Asp Ile Glu Ala Ala Gly Arg Ala 225 230 235 240
- Val Val Lys Met Leu Glu Leu Gly Leu Lys Pro Ser Asp Ile Leu Thr 245 250 255
- Arg Glu Ala Phe Glu Asp Ala Ile Thr Val Thr Met Ala Leu Gly Gly 260 265 270
- Ser Thr Asn Ala Thr Leu His Leu Leu Ala Ile Ala His Ala Ala Asn 275 280 285
- Val Asp Leu Ser Leu Glu Asp Phe Asn Thr Ile Gln Glu Arg Val Pro 290 295 300
- His Leu Ala Asp Leu Lys Pro Ser Gly Gln Tyr Val Phe Gln Asp Leu 305 310 315 320
- Tyr Glu Val Gly Gly Val Pro Ala Val Met Lys Tyr Leu Leu Ala Asn 325 330 335
- Gly Phe Leu His Gly Asp Arg Ile Thr Cys Thr Gly Lys Thr Val Ala 340 345 350
- Glu Asn Leu Ala Asp Phe Ala Asp Leu Thr Pro Gly Gln Lys Val Ile 355 360 365
- Met Pro Leu Glu Asn Pro Lys Arg Ala Asp Gly Pro Leu Ile Ile Leu 370 375 380
- Asn Gly Asn Leu Ala Pro Asp Gly Ala Val Ala Lys Val Ser Gly Val 385 390 395 400
- Lys Val Arg Arg His Val Gly Pro Ala Lys Val Phe Asp Ser Glu Glu 405 410 415
- Asp Ala Ile Gln Ala Val Leu Thr Asp Glu Ile Val Asp Gly Asp Val 420 425 430
- Val Val Arg Phe Val Gly Pro Lys Gly Gly Pro Gly Met Pro Glu 435 440 445
- Met Leu Ser Leu'Ser Ser Met Ile Val Gly Lys Gly Gln Gly Asp Lys 450 455 460
- Val Ala Leu Leu Thr Asp Gly Arg Phe Ser Gly Gly Thr Tyr Gly Leu 465 470 475 480
- Val Val Gly His Ile Ala Pro Glu Ala Gln Asp Gly Gly Pro Ile Ala 485 490 495

Tyr Leu Arg Thr Gly Asp Ile Val Thr Val Asp Gln Asp Thr Lys Glu 510

Ile Ser Met Ala Val Ser Glu Glu Glu Leu Glu Lys Arg Lys Ala Glu 520

Thr Thr Leu Pro Pro Leu Tyr Ser Arg Gly Val Leu Gly Lys Tyr Ala 530

His Ile Val Ser Ser Ala Ser Arg Gly Ala Val Thr Asp Phe Trp Asn

555

Met Asp Lys Ser Gly Lys Lys

550

<210> 53 <211> 274

<212> DNA

<213> Streptococcus pneumoniae

<400> 53

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<211> 91

<212> PRT

<213> Streptococcus pneumoniae

<400> 54

Cys Tyr Asn Lys Asn Lys Glu Phe Lys Glu Lys Tyr Asn Met Ser Ile
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Phe Ile Gly Gly Ala Trp Pro Tyr Ala Asn Gly Ser Leu His Ile Gly
20 25 30

His Ala Ala Ala Leu Leu Pro Gly Asp Ile Leu Ala Arg Tyr Tyr Arg

Gln Lys Gly Glu Glu Val Leu Tyr Val Ser Gly Ser Asp Cys Asn Gly
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Thr Pro Ile Ser Ile Arg Ala Lys Lys Glu Asn Lys Ser Val Lys Glu
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Ile Ala Asp Phe Tyr His Lys Glu Phe Asn Pro 85 90

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gtaccagata gttctgcaat tttgacagcc aatgaaaaaa atatcatctc aaaagcttgg 540
qataaccgct acggtgtcct catggtaagc gagctagctg aagctttatc gggtcaaaaa 600
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cataceteta caaceaagtt tgacecagaa gtetteeteg cagttgattg etcaceagea 720
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ggtatcaagt accaatacta ctgtggtaaa ggcggaacag atgcaggtgc agctcatctg 900
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caaaccctct atgcaatgga tgacttccta gaagcgcaag ctttcttaca agccttggtg 1020
aagaaattgg atcgttcaac ggttgatttg attaaacatt attaa
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<212> PRT
<213> Streptococcus pneumoniae
<400> 56
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Val Ser Gly His Glu Ala Pro Val Arg Ala Tyr Leu Arg Glu Lys Leu
                                  25
 Thr Pro His Val Asp Glu Val Val Thr Asp Gly Leu Gly Gly Ile Phe
                              40
         35
Gly Ile Lys His Ser Glu Ala Val Asp Ala Pro Arg Val Leu Val Ala
 Ser His Met Asp Glu Val Gly Phe Met Val Ser Glu Ile Lys Pro Asp
                      70
  65
 Gly Thr Phe Arg Val Val Glu Ile Gly Gly Trp Asn Pro Met Val Val
 Ser Ser Gln Arg Phe Lys Leu Leu Thr Arg Asp Gly His Glu Ile Pro
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1065

140

105

Val Ile Ser Gly Ser Val Pro Pro His Leu Thr Arg Gly Lys Gly Gly 120

Pro Thr Met Pro Ala Ile Ala Asp Ile Val Phe Asp Gly Gly Phe Ala

135

100

115

130

Asp Lys Ala Glu Ala Glu Ser Phe Gly Ile Arg Pro Gly Asp Thr Ile 145 Val Pro Asp Ser Ser Ala Ile Leu Thr Ala Asn Glu Lys Asn Ile Ile 170 Ser Lys Ala Trp Asp Asn Arg Tyr Gly Val Leu Met Val Ser Glu Leu 185 Ala Glu Ala Leu Ser Gly Gln Lys Leu Gly Asn Glu Leu Tyr Leu Gly Ser Asn Val Gln Glu Glu Val Gly Leu Arg Gly Ala His Thr Ser Thr 215 210 Thr Lys Phe Asp Pro Glu Val Phe Leu Ala Val Asp Cys Ser Pro Ala 230 Gly Asp Val Tyr Gly Gly Gln Gly Lys Ile Gly Asp Gly Thr Leu Ile Arg Phe Tyr Asp Pro Gly His Leu Leu Pro Gly Met Lys Asp Phe 265 260 Leu Leu Thr Thr Ala Glu Glu Ala Gly Ile Lys Tyr Gln Tyr Tyr Cys 280 Gly Lys Gly Gly Thr Asp Ala Gly Ala Ala His Leu Lys Asn Gly Gly 290 Val Pro Ser Thr Thr Ile Gly Val Cys Ala Arg Tyr Ile His Ser His 305 310 Gln Thr Leu Tyr Ala Met Asp Asp Phe Leu Glu Ala Gln Ala Phe Leu Gln Ala Leu Val Lys Lys Leu Asp Arg Ser Thr Val Asp Leu Ile Lys 350 345 340

His Tyr

<210> 57 <211> 1182 <212> DNA <213> Streptococcus pneumoniae

<400> 57
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agcctatctc tgacttttat cctagccact cgtctccac tactagaaag ctggtttcac 180
agtttggaga aggtctacac cgtccacaaa ttcacagcct ttctctcaat catcctacta 240
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caatacgaag cttggcgatg gattcaccgc ctggtttacc tagcctatat tttaggactc 420 tttcacatct acatgataat gggcaatcgt ctccttacat ttaatcttct aagttttctt 480 gttggtagct atgccctttt aggcttacta gctggttttt atatcatttt tctatatcaa 540 aagattteet teeeetatet agggaaaatt acceatetea aaegettaaa teaegataet 600 agagaaattc aaatccatct tagcagacct ttcaactatc aatcaggaca atttgccttt 660 ctaaagattt tccaagaagg ctttgaaagt gctccgcatc ccttttctat ctcaggaggt 720 catggtcaaa ctctttactt tactgttaaa acttcaggcg accataccaa gaatatctat 780 qataatcttc aagccggcag caaagtaacc ctagacagag cttacggaca catgatcata 840 gaagaaggac gagaaaatca ggtttggatt gctggaggta ttgggatcac ccccttcatc 900 tettacatee gtgaacatee tattttagat aaacaggtte aettetaeta tagetteegt 960 qqaqatgaaa atgcagtcta cctagattta ctccgtaact atgctcagaa aaatcctaat 1020 tttgaactcc atctaatcga cagtacgaaa gacggctatc ttaattttga acaaaaagaa 1080 gtgcccgaac atgcaaccgt ctatatgtgt ggtcctattt ctatgatgaa ggcacttgcc 1140 aaacagatta agaaacaaaa tccaaaaaca gagcatattt ac 1182 <210> 58 <211> 394 <212> PRT <213> Streptococcus pneumoniae

<400> 58

Met Glu Phe Ser Met Lys Ser Val Lys Gly Leu Leu Phe Ile Ile Ala 1 5 10 15

Ser Phe Ile Leu Thr Leu Leu Thr Trp Met Asn Thr Ser Pro Gln Phe 20 25 30

Met Ile Pro Gly Leu Ala Leu Thr Ser Leu Ser Leu Thr Phe Ile Leu 35 40 45

Ala Thr Arg Leu Pro Leu Leu Glu Ser Trp Phe His Ser Leu Glu Lys
50 55 60

Val Tyr Thr Val His Lys Phe Thr Ala Phe Leu Ser Ile Ile Leu Leu 65 70 75 80

Ile Phe His Asn Phe Ser Met Gly Gly Leu Trp Gly Ser Arg Leu Ala 85 90 95

Ala Gln Phe Gly Asn Leu Ala Ile Tyr Ile Phe Ala Ser Ile Ile Leu 100 105 110

Val Ala Tyr Leu Gly Lys Tyr Ile Gln Tyr Glu Ala Trp Arg Trp Ile 115 120 125

His Arg Leu Val Tyr Leu Ala Tyr Ile Leu Gly Leu Phe His Ile Tyr 130 135 140

Met Ile Met Gly Asn Arg Leu Leu Thr Phe Asn Leu Leu Ser Phe Leu 145 150 155 160

Val Gly Ser Tyr Ala Leu Leu Gly Leu Leu Ala Gly Phe Tyr Ile Ile 165 170 175

Phe Leu Tyr Gln Lys Ile Ser Phe Pro Tyr Leu Gly Lys Ile Thr His 180 185 190 Leu Lys Arg Leu Asn His Asp Thr Arg Glu Ile Gln Ile His Leu Ser Arg Pro Phe Asn Tyr Gln Ser Gly Gln Phe Ala Phe Leu Lys Ile Phe 210 Gln Glu Gly Phe Glu Ser Ala Pro His Pro Phe Ser Ile Ser Gly Gly 235 225 His Gly Gln Thr Leu Tyr Phe Thr Val Lys Thr Ser Gly Asp His Thr 250 Lys Asn Ile Tyr Asp Asn Leu Gln Ala Gly Ser Lys Val Thr Leu Asp 265 Arg Ala Tyr Gly His Met Ile Ile Glu Glu Gly Arg Glu Asn Gln Val 280 Trp Ile Ala Gly Gly Ile Gly Ile Thr Pro Phe Ile Ser Tyr Ile Arg 300 295 Glu His Pro Ile Leu Asp Lys Gln Val His Phe Tyr Tyr Ser Phe Arg 315 305 310 Gly Asp Glu Asn Ala Val Tyr Leu Asp Leu Leu Arg Asn Tyr Ala Gln 330 Lys Asn Pro Asn Phe Glu Leu His Leu Ile Asp Ser Thr Lys Asp Gly Tyr Leu Asn Phe Glu Gln Lys Glu Val Pro Glu His Ala Thr Val Tyr 355 360 Met Cys Gly Pro Ile Ser Met Met Lys Ala Leu Ala Lys Gln Ile Lys 375

Lys Gln Asn Pro Lys Thr Glu His Ile Tyr 385 390

<210> 59 <211> 900 <212> DNA <213> Streptococcus pneumoniae

<400> 59

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atcacagacc atccagaacg tttcttggtt tcagaaatgg ttcgcgagaa agtcttgcac 600 ctaactcgtg aagagattcc gcattctgta gcagtagttg ttgactctat gaaacgagac 660 gaagagacag acaaggttca catccgtgca accatcatgg tcgagcgcga tagccaaaaa 720 gggattatca tcggtaaagg tggcgctatg cttaagaaaa tcggtagcat ggcccgtcgt 780 gatatcgaac tcatgctagg agacaaggtc ttcctagaaa cctgggtcaa ggtcaagaaa 840 aactggcgcg ataaaaaagct agatttggct gactttggct ataatgaaag agaatactaa 900 <210> 60 <211> 299 <212> PRT <213> Streptococcus pneumoniae

Gly Lys Ser Thr Phe Leu Asn His Val Met Gly Gln Lys Ile Ala Ile 20 25 30

Met Ser Asp Lys Ala Gln Thr Thr Arg Asn Lys Ile Met Gly Ile Tyr 35 40 45

Thr Thr Asp Lys Glu Gln Ile Val Phe Ile Asp Thr Pro Gly Ile His
50 55 60

Lys Pro Lys Thr Ala Leu Gly Asp Phe Met Val Glu Ser Ala Tyr Ser 65 70 75 80

Thr Leu Arg Glu Val Asp Thr Val Leu Phe Met Val Pro Ala Asp Glu 85 90 95

Ala Arg Gly Lys Gly Asp Asp Met Ile Ile Glu Arg Leu Lys Ala Ala 100 105 110

Lys Val Pro Val Ile Leu Val Val Asn Lys Ile Asp Lys Val His Pro 115 120 125

Asp Gln Leu Leu Ser Gln Ile Asp Asp Phe Arg Asn Gln Met Asp Phe 130 135 140

Leu Val Asp Ile Leu Ser Glu Asn Leu Asp Glu Gly Phe Gln Tyr Phe 165 170 175

Pro Ser Asp Gln Ile Thr Asp His Pro Glu Arg Phe Leu Val Ser Glu 180 185 190

Met Val Arg Glu Lys Val Leu His Leu Thr Arg Glu Glu Ile Pro His 195 200 205

Ser Val Ala Val Val Val Asp Ser Met Lys Arg Asp Glu Glu Thr Asp

Lys Val His Ile Arg Ala Thr Ile Met Val Glu Arg Asp Ser Gln Lys

Gly Ile Ile Ile Gly Lys Gly Gly Ala Met Leu Lys Lys Ile Gly Ser 245 250 255

Met Ala Arg Arg Asp Ile Glu Leu Met Leu Gly Asp Lys Val Phe Leu 260 265 270

Glu Thr Trp Val Lys Val Lys Lys Asn Trp Arg Asp Lys Lys Leu Asp 275 280 285

Leu Ala Asp Phe Gly Tyr Asn Glu Arg Glu Tyr 290 295

<210> 61

<211> 855

<212> DNA

<213> Streptococcus pneumoniae

<400> 61

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<211> 284

<212> PRT

<213> Streptococcus pneumoniae

<400> 62

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Val Glu Thr Val Cys Arg Gly Leu Glu Lys Leu Ile Ile Gly Lys Lys
20 25 30

Ile Ser Ser Ile Glu Ile Arg Tyr Pro Lys Met Ile Lys Thr Asp Leu 35 40 45

Glu Glu Phe Gln Arg Glu Leu Pro Ser Gln Ile Ile Glu Ser Met Gly 50 55 60

Arg Arg Gly Lys Tyr Leu Leu Phe Tyr Leu Thr Asp Lys Val Leu Ile Ser His Leu Arg Met Glu Gly Lys Tyr Phe Tyr Tyr Pro Asp Gln Gly Pro Glu Arg Lys His Ala His Val Phe Phe His Phe Glu Asp Gly Gly 105 110 100 Thr Leu Val Tyr Glu Asp Val Arg Lys Phe Gly Thr Met Glu Leu Leu 120 115 Val Pro Asp Leu Leu Asp Val Tyr Phe Ile Ser Lys Lys Leu Gly Pro 135 Glu Pro Ser Glu Gln Asp Phe Asp Leu Gln Val Phe Gln Ser Ala Leu 155 145 Ala Lys Ser Lys Lys Pro Ile Lys Ser His Leu Leu Asp Gln Thr Leu 170 Val Ala Gly Leu Gly Asn Ile Tyr Val Asp Glu Val Leu Trp Arg Ala 185 Gln Val His Pro Ala Arg Pro Ser Gln Thr Leu Thr Ala Glu Glu Ala 205 200 195 Thr Ala Ile His Asp Gln Thr Ile Ala Val Leu Gly Gln Ala Val Glu 215 Lys Gly Gly Ser Thr Ile Arg Thr Tyr Thr Asn Ala Phe Gly Glu Asp 225 Gly Ser Met Gln Asp Phe His Gln Val Tyr Asp Lys Thr Gly Gln Glu 250

Cys Val Arg Cys Gly Thr Ile Ile Glu Lys Ile Gln Leu Gly Gly Arg 265

Gly Thr His Phe Cys Pro Asn Cys Gln Arg Arg Asp 280 275

<210> 63

<211> 633

<212> DNA

<213> Streptococcus pneumoniae

<400> 63

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<210> 64

<211> 210

<212> PRT

<213> Streptococcus pneumoniae

<400> 64

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Thr Gly Gly Ile Ala Ser Gly Lys Ser Thr Val Thr Asn Phe Leu Arg
20 25 30

Gln Gln Gly Phe Gln Val Val Asp Ala Asp Ala Val Val His Gln Leu
35 40 45

Gln Lys Pro Gly Gly Arg Leu Phe Glu Ala Leu Val Gln His Phe Gly 50 55 60

Gln Glu Ile Ile Leu Glu Asn Gly Glu Leu Asn Arg Pro Leu Leu Ala 65 70 75 80

Ser Leu Ile Phe Ser Asn Pro Asp Glu Arg Glu Trp Ser Lys Gln Ile 85 90 95

Gln Gly Glu Ile Ile Arg Glu Glu Leu Ala Thr Leu Arg Glu Gln Leu 100 105 110

Ala Gln Thr Glu Glu Ile Phe Phe Met Asp Ile Pro Leu Leu Phe Glu 115 120 125

Gln Asp Tyr Ser Asp Trp Phe Ala Glu Thr Trp Leu Val Tyr Val Asp

Arg Asp Ala Gln Val Glu Arg Leu Met Lys Arg Asp Gln Leu Ser Lys 145 150 155 160

Asp Glu Ala Glu Ser Arg Leu Ala Ala Gln Trp Pro Leu Glu Lys Lys 165 170 175

Lys Asp Leu Ala Ser Gln Val Leu Asp Asn Asn Gly Asn Gln Asn Gln
180 185 190

Leu Leu Asn Gln Val His Ile Leu Leu Glu Gly Gly Arg Gln Asp Asp 195 200 205

Arg Asp 210

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Tyr Gly Arg Lys Pro Met Met Ile Arg Ala Gly Leu Ala Met Thr Ile 100 105 110

Ile Ser Ala Ala Leu Phe Ser Pro Ile Trp Gly Ile Leu Ala Asp Lys

Thr Met Gly Gly Leu Ala Phe Val Pro Asn Ile Tyr Trp Leu Ile Phe

115 120 125

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Ala Leu Ile Ala Ser Gln Val Pro Lys Glu Lys Ser Gly Ser Ala Leu 145 150 155 160

Gly Thr Leu Ser Thr Gly Val Val Ala Gly Thr Leu Thr Gly Pro Phe 165 170 175

Ile Gly Gly Phe Ile Ala Glu Leu Phe Gly Ile Arg Thr Val Phe Leu 180 185 190

Leu Val Gly Ser Phe Leu Phe Leu Ala Ala Ile Leu Thr Ile Cys Phe 195 200 205

Ile Lys Glu Asp Phe Gln Pro Val Ala Lys Glu Lys Ala Ile Pro Thr 210 215 220

Lys Glu Leu Phe Thr Ser Val Lys Tyr Pro Tyr Leu Leu Leu Asn Leu 225 230 235 240

Phe Leu Thr Ser Phe Val Ile Gln Phe Ser Ala Gln Ser Ile Gly Pro 245 250 255

Ile Leu Ala Leu Tyr Val Arg Asp Leu Gly Gln Thr Glu Asn Leu Leu 260 265 270

Phe Val Ser Gly Leu Ile Val Ser Ser Met Gly Phe Ser Ser Met Met 275 280 285

Ser Ala Gly Val Met Gly Lys Leu Gly Asp Lys Val Gly Asn His Arg 290 295 300

Leu Leu Val Val Ala Gln Phe Tyr Ser Val Ile Ile Tyr Leu Leu Cys 305 310 315 320

Ala Asn Ala Ser Ser Pro Leu Gln Leu Gly Leu Tyr Arg Phe Leu Phe 325 330 335

Gly Leu Gly Thr Gly Ala Leu Ile Pro Gly Val Asn Ala Leu Leu Ser 340 345 350

Lys Met Thr Pro Lys Ala Gly Ile Ser Arg Val Phe Ala Phe Asn Gln 355 360 365

Val Phe Phe Tyr Leu Gly Gly Val Val Gly Pro Met Ala Gly Ser Ala 370 375 380

Val Ala Gly Gln Phe Gly Tyr His Ala Val Phe Tyr Ala Thr Ser Leu 385 390 395 400

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Leu Asn Arg Ser Phe Ser Met Ile Asp Thr Gly Gly Ile Asp Asp Val
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Asp Ala Pro Phe Met Glu Gln Ile Lys His Gln Ala Glu Ile Ala Met
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 Glu Glu Ala Asp Val Ile Val Phe Val Val Ser Gly Lys Glu Gly Ile
                  85
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Thr Asp Ala Asp Glu Tyr Val Ala Arg Lys Leu Tyr Lys Thr His Lys
100 105 110

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- Asp Ile Tyr Asp Phe Tyr Ala Leu Gly Leu Gly Glu Pro Leu Pro Ile 130 135 140
- Ser Ser Val His Gly Ile Gly Thr Gly Asp Val Leu Asp Ala Ile Val 145 150 155 160
- Glu Asn Leu Pro Asn Glu Tyr Glu Glu Glu Asn Pro Asp Val Ile Lys 165 170 175
- Phe Ser Leu Ile Gly Arg Pro Asn Val Gly Lys Ser Ser Leu Ile Asn 180 185 190
- Ala Ile Leu Gly Glu Asp Arg Val Ile Ala Ser Pro Val Ala Gly Thr 195 200 205
- Thr Arg Asp Ala Ile Asp Thr His Phe Thr Asp Thr Asp Gly Gln Glu 210 215 220
- Phe Thr Met Ile Asp Thr Ala Gly Met Arg Lys Ser Gly Lys Val Tyr 225 230 235 240
- Glu Asn Thr Glu Lys Tyr Ser Val Met Arg Ala Met Arg Ala Ile Asp 245 250 255
- Arg Ser Asp Val Val Leu Met Val Ile Asn Ala Glu Glu Gly Ile Arg 260 265 270
- Glu Tyr Asp Lys Arg Ile Ala Gly Phe Ala His Glu Ala Gly Lys Gly 275 280 285
- Met Ile Ile Val Val Asn Lys Trp Asp Thr Leu Glu Lys Asp Asn His 290 295 300
- Thr Met Lys Asn Trp Glu Glu Asp Ile Arg Glu Gln Phe Gln Tyr Leu 305 310 315 320
- Pro Tyr Ala Pro Ile Ile Phe Val Ser Ala Leu Thr Lys Gln Arg Leu 325 330 335
- His Lys Leu Pro Glu Met Ile Lys Gln Ile Ser Glu Ser Gln Asn Thr 340 345 350
- Arg Ile Pro Ser Ala Val Leu Asn Asp Val Ile Met Asp Ala Ile Ala 355 360 365
- Ile Asn Pro Thr Pro Thr Asp Lys Gly Lys Arg Leu Lys Ile Phe Tyr 370 375 380
- Ala Thr Gln Val Ala Thr Lys Pro Pro Thr Phe Val Ile Phe Val Asn 385 390 395 400

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Gln Pro Gln Gly Val Glu Gly Leu Leu Ile Ser Ser Val Asp Ala Ala

100 105 110

Leu Ala Gly Gln Asn Ala Leu Leu Ala Ala Glu Ser Leu Gly Tyr Gly 125 115 120 Gly Val Ile Ile Gly Leu Val Arg Tyr Lys Ser Glu Glu Val Ala Glu 140 135 Leu Phe Asn Leu Pro Asp Tyr Thr Tyr Ser Val Phe Gly Met Ala Leu 155 150 145 Gly Val Pro Asn Gln His His Asp Met Lys Pro Arg Leu Pro Leu Glu 170 165 Asn Val Val Phe Glu Glu Glu Tyr Gln Glu Gln Ser Thr Glu Ala Ile 185 Gln Ala Tyr Asp Arg Val Gln Ala Asp Tyr Ala Gly Ala Arg Ala Thr 195 Thr Ser Trp Ser Gln Arg Leu Ala Glu Gln Phe Gly Gln Ala Glu Pro Ser Ser Thr Arg Lys Asn Leu Glu Gln Lys Lys Leu Leu 230 235 225 <210> 71 <211> 729 <212> DNA <213> Streptococcus pneumoniae <400> 71 atgacagaaa ttagactaga gcacgtcagt tatgcctatg gtcaggagag gattttagag 60 gatatcaacc tacaggtgac ttcaggcgaa gtggtttcca tcctaggccc aagtggtgtt 120 ggaaagacca ccctctttaa tctaatcgct gggattttag aagttcagtc agggagaatt 180 qtccttgatg gtgaagaaaa tcccaagggg cgcgtgagtt atatgttgca aaaggatctg 240 ctcttggagc acaagacggt gcttggaaat atcattctgc ccctcttgat tcaaaaggtg 300 gataaggcag aagctatttc ccgagcggat aaaattcttg cgaccttcca gctgacagct 360 gtaagagaca agtateetea tgaaettage ggtgggatge geeagegtgt ageettaete 420 cggacctacc tttttgggca caagctcttt ctcttagatg aggcctttag cgccttggat 480 gagatgacaa agatggaact ccacgcttgg tatcttgaga ttcacaagca gttgcagcta 540 acaaccctga tcatcacgca tagtattgag gaggccctca atctcagcga ccgtatctat 600 atcttgaaaa atcgccctgg gcagattgtt tcagaaatta aactagattg gtctgaagat 660 gaggacaagg aagtccaaaa gattgcctac aaacgtcaaa ttttggcgga attaggctta 720 729 gataagtag <210> 72 <211> 242 <212> PRT <213> Streptococcus pneumoniae <400> 72 Met Thr Glu Ile Arg Leu Glu His Val Ser Tyr Ala Tyr Gly Gln Glu

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Ile Ala Gly Ile Leu Glu Val Gln Ser Gly Arg Ile Val Leu Asp Gly 50 55 60

Glu Glu Asn Pro Lys Gly Arg Val Ser Tyr Met Leu Gln Lys Asp Leu
65 70 75 80

Leu Leu Glu His Lys Thr Val Leu Gly Asn Ile Ile Leu Pro Leu Leu 85 90 95

Ile Gln Lys Val Asp Lys Ala Glu Ala Ile Ser Arg Ala Asp Lys Ile 100 105 110

Leu Ala Thr Phe Gln Leu Thr Ala Val Arg Asp Lys Tyr Pro His Glu 115 120 125

Leu Ser Gly Gly Met Arg Gln Arg Val Ala Leu Leu Arg Thr Tyr Leu 130 135 140

Phe Gly His Lys Leu Phe Leu Leu Asp Glu Ala Phe Ser Ala Leu Asp 145 150 155 160

Glu Met Thr Lys Met Glu Leu His Ala Trp Tyr Leu Glu Ile His Lys 165 170 175

Gln Leu Gln Leu Thr Thr Leu Ile Ile Thr His Ser Ile Glu Glu Ala 180 185 190

Leu Asn Leu Ser Asp Arg Ile Tyr Ile Leu Lys Asn Arg Pro Gly Gln
195 200 205

Ile Val Ser Glu Ile Lys Leu Asp Trp Ser Glu Asp Glu Asp Lys Glu 210 215 220

Val Gln Lys Ile Ala Tyr Lys Arg Gln Ile Leu Ala Glu Leu Gly Leu 225 230 235 240

Asp Lys

<210> 73

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<213> Streptococcus pneumoniae

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Ile Ala Met Ser Asn His Ser Tyr Ser Val Ala Gly Ala Thr Leu Asn 35 40 45

Asp Tyr Pro Tyr Glu Met Asp Arg Leu Glu Glu Val Ala Leu Glu Leu
50 55 60

- Thr Glu Thr Asp Tyr Ser Gln Asp Glu Thr Phe Thr Glu Leu Pro Phe
 65 70 75 80
- Ser Arg Arg Leu Gln Val Leu Phe Asp Glu Ala Glu Tyr Val Ala Ser 85 90 95
- Val Val His Ala Lys Val Leu Gly Thr Glu His Val Leu Tyr Ala Ile 100 105 110
- Leu His Asp Ser Asn Ala Leu Ala Thr Arg Ile Leu Glu Arg Ala Gly
 115 120 125
- Phe Ser Tyr Glu Asp Lys Lys Asp Gln Val Lys Ile Ala Ala Leu Arg 130 135 140
- Arg Asn Leu Glu Glu Arg Ala Gly Trp Thr Arg Glu Asp Leu Lys Ala 145 150 155 160
- Leu Arg Gln Arg His Arg Thr Val Ala Asp Lys Gln Asn Ser Met Ala 165 170 175
- Asn Met Met Gly Met Pro Gln Thr Pro Ser Gly Gly Leu Glu Asp Tyr
- Thr His Asp Leu Thr Glu Gln Ala Arg Ser Gly Lys Leu Glu Pro Val
- Ile Gly Arg Asp Lys Glu Ile Ser Arg Met Ile Gln Ile Leu Ser Arg 210 215 220
- Lys Thr Lys Asn Asn Pro Val Leu Val Gly Asp Ala Gly Val Gly Lys 225 230 235
- Thr Ala Leu Ala Leu Gly Leu Ala Gln Arg Ile Ala Ser Gly Asp Val 245 250 255
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- Val Val Ala Gly Thr Arg Phe Arg Gly Asp Phe Glu Glu Arg Met Asn 275 280 285
- Asn Ile Ile Lys Asp Ile Glu Glu Asp Gly Gln Val Ile Leu Phe Ile 290 295 300
- Asp Glu Leu His Thr Ile Met Gly Ser Gly Ser Gly Ile Asp Ser Thr 305 310 315 320
- Leu Asp Ala Ala Asn Ile Leu Lys Pro Ala Leu Ala Arg Gly Thr Leu 325 330 335
- Arg Thr Val Gly Ala Thr Thr Gln Glu Glu Tyr Gln Lys His Ile Glu 340 345 350
- Lys Asp Ala Ala Leu Ser Arg Arg Phe Ala Lys Val Thr Ile Glu Glu 355 360 365

- Pro Ser Val Ala Asp Ser Met Thr Ile Leu Gln Gly Leu Lys Ala Thr 370 380
- Tyr Glu Lys His His Arg Val Gln Ile Thr Asp Glu Ala Val Glu Thr 385 390 395 400
- Ala Val Lys Met Ala His Arg Tyr Leu Thr Ser Arg His Leu Pro Asp 405 410 415
- Ser Ala Ile Asp Leu Leu Asp Glu Ala Ala Ala Thr Val Gln Asn Lys 420 425 430
- Ala Lys His Val Lys Ala Asp Asp Ser Asp Leu Ser Pro Ala Asp Lys 435 440 445
- Ala Leu Met Asp Gly Lys Trp Lys Gln Ala Ala Gln Leu Ile Ala Lys 450 455 460
- Glu Glu Glu Val Pro Val Tyr Lys Asp Leu Val Thr Glu Ser Asp Ile 465 470 475 480
- Leu Thr Thr Leu Ser Arg Leu Ser Gly Ile Pro Val Gln Lys Leu Thr 485 490 495
- Gln Thr Asp Ala Lys Lys Tyr Leu Asn Leu Glu Ala Glu Leu His Lys 500 505 510
- Arg Val Ile Gly Gln Asp Gln Ala Val Ser Ser Ile Ser Arg Ala Ile 515 520 525
- Arg Arg Asn Gln Ser Gly Ile Arg Ser His Lys Arg Pro Ile Gly Ser
- Phe Met Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Glu Leu Ala Lys 545 550 555 560
- Ala Leu Ala Glu Val Leu Phe Asp Asp Glu Ser Ala Leu Ile Arg Phe 565 570 575
- Asp Met Ser Glu Tyr Met Glu Lys Phe Ala Ala Ser Arg Leu Asn Gly 580 585 590
- Ala Pro Pro Gly Tyr Val Gly Tyr Glu Glu Gly Gly Glu Leu Thr Glu
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- Lys Val Arg Asn Lys Pro Tyr Ser Val Leu Leu Phe Asp Glu Val Glu 610 615 620
- Lys Ala His Pro Asp Ile Phe Asn Val Leu Gln Val Leu Asp Asp 625 630 635 640
- Gly Val Leu Thr Asp Ser Lys Gly Arg Lys Val Asp Phe Ser Asn Thr 645 650 655
- Ile Ile Ile Met Thr Ser Asn Leu Gly Ala Thr Ala Leu Arg Asp Asp 660 665 670

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Asn Thr Asn His Thr Gly Leu Tyr Val Ala Lys Glu Lys Gly Tyr Phe
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Lys Glu Ala Gly Val Asp Val Asp Leu Lys Leu Pro Pro Glu Glu Ser 65 70 75 80

Ser Ser Asp Leu Val Ile Asn Gly Lys Ala Pro Phe Ala Val Tyr Phe 85 90 95

Gln Asp Tyr Met Ala Lys Lys Leu Glu Lys Gly Ala Gly Ile Thr Ala 100 105 110

Val Ala Ala Ile Val Glu His Asn Thr Ser Gly Ile Ile Ser Arg Lys 115 120 125

Ser Asp Asn Val Ser Ser Pro Lys Asp Leu Val Gly Lys Lys Tyr Gly 130 135 140

Thr Trp Asn Asp Pro Thr Glu Leu Ala Met Leu Lys Thr Leu Val Glu 145 150 155 160

Ser Gln Gly Gly Asp Phe Glu Lys Val Glu Lys Val Pro Asn Asn Asp 165 170 175

Ser Asn Ser Ile Thr Pro Ile Ala Asn Gly Val Phe Asp Thr Ala Trp 180 185 190

Ile Tyr Tyr Gly Trp Asp Gly Ile Leu Ala Lys Ser Gln Gly Val Asp 195 200 205

Ala Asn Phe Met Tyr Leu Lys Asp Tyr Val Lys Glu Phe Asp Tyr Tyr 210 215 220

Ser Pro Val Ile Ile Ala Asn Asn Asp Tyr Leu Lys Asp Asn Lys Glu 225 230 235 240

Glu Ala Arg Lys Val Ile Gln Ala Ile Lys Lys Gly Tyr Gln Tyr Ala 245 250 255

Met Glu His Pro Glu Glu Ala Ala Asp Ile Leu Ile Lys Asn Ala Pro 260 265 270

Glu Leu Lys Glu Lys Arg Asp Phe Val Ile Glu Ser Gln Lys Tyr Leu 275 280 285 Ser Lys Glu Tyr Ala Ser Asp Lys Glu Lys Trp Gly Gln Phe Asp Ala 295 290 Ala Arg Trp Asn Ala Phe Tyr Lys Trp Asp Lys Glu Asn Gly Ile Leu 320 310 315 Lys Glu Asp Leu Thr Asp Lys Gly Phe Thr Asn Glu Phe Val Lys 330 325 <210> 77 <211> 762 <212> DNA <213> Streptococcus pneumoniae <400> 77 ttgatgagaa acttgagaag tatactgaga cgacacatta gtctattggg ctttctcgga 60 gtattgtcaa totggcagtt agcaggtttt ottaaactto tooccaagtt tatcotgcog 120 acacctettg aaatteteea geeetttgtt egtgacagag aatttetetg geaccatage 180 tgggcgacct tgagagtggc tttactgggg ctgattttgg gagttttgat tgcctgtctt 240 atggctgtgc tcatggatag tttgacttgg ctcaatgacc tgatttaccc tatgatggtg 300 gtcattcaga ccattccgac cattgccata gctcctatcc tggtcttgtg gctaggttat 360 qqqattttgc ccaagattgt cttgattatc ttaacgacaa cctttcccat catcgttagt 420 attttggacg gttttaggca ttgcgacaag gatatgctga ccttgtttag tctgatgcgg 480 gccaagcett ggcaaateet gtggcatttt aaaateecag ttageetgee ttaettttat 540 qcaggtctga gggtcagtgt ctcctacgcc tttatcacaa ctgtggtatc tgagtggttg 600 ggaggttttg aaggtcttgg tgtttatatg attcagtcta aaaaactgtt tcagtatgat 660 accatgtttg ccattattat tctggtgtcg attatcagtc ttttgggtat gaagctggtc 720 gatatcagtg aaaaatatgt gattaaatgg aaacgttcgt ag <210> 78 <211> 253 <212> PRT <213> Streptococcus pneumoniae <400> 78 Met Met Arg Asn Leu Arg Ser Ile Leu Arg Arg His Ile Ser Leu Leu 10 1 Gly Phe Leu Gly Val Leu Ser Ile Trp Gln Leu Ala Gly Phe Leu Lys 25 Leu Leu Pro Lys Phe Ile Leu Pro Thr Pro Leu Glu Ile Leu Gln Pro 40 Phe Val Arg Asp Arg Glu Phe Leu Trp His His Ser Trp Ala Thr Leu 55 Arg Val Ala Leu Leu Gly Leu Ile Leu Gly Val Leu Ile Ala Cys Leu 70 Met Ala Val Leu Met Asp Ser Leu Thr Trp Leu Asn Asp Leu Ile Tyr

90

Pro Met Met Val Val Ile Gln Thr Ile Pro Thr Ile Ala Ile Ala Pro 105 100 Ile Leu Val Leu Trp Leu Gly Tyr Gly Ile Leu Pro Lys Ile Val Leu 120 Ile Ile Leu Thr Thr Thr Phe Pro Ile Ile Val Ser Ile Leu Asp Gly 135 Phe Arg His Cys Asp Lys Asp Met Leu Thr Leu Phe Ser Leu Met Arg 155 145 Ala Lys Pro Trp Gln Ile Leu Trp His Phe Lys Ile Pro Val Ser Leu 170 Pro Tyr Phe Tyr Ala Gly Leu Arg Val Ser Val Ser Tyr Ala Phe Ile 185 180 Thr Thr Val Val Ser Glu Trp Leu Gly Gly Phe Glu Gly Leu Gly Val 200 Tyr Met Ile Gln Ser Lys Lys Leu Phe Gln Tyr Asp Thr Met Phe Ala 215 Ile Ile Ile Leu Val Ser Ile Ile Ser Leu Leu Gly Met Lys Leu Val 240 230 235 225 Asp Ile Ser Glu Lys Tyr Val Ile Lys Trp Lys Arg Ser 250 245 <210> 79 <211> 372 <212> DNA <213> Streptococcus pneumoniae <400> 79 ttgattttta atcctatttg ctgtatgata agggaaaaga aaggggacag agatatggct 60 tttaccaata cccacatgcg atctgctagt tttggtattg ttaccagctt gcctgatgac 120 atcattgact ctttttggta tatcatcgac catttcttaa aaaatgtctt tgaattggaa 180 gaagaactcg agtttcaatt gcttaataac caaggaaaga ttaccttcca cttttcaagt 240 caacacctcc ctacagccat tgattttgac tttaaccatc ctttcgaccc tcgttatccc 300 ccaagagtac tggttttaga catggacggt agagaaacta tcctcctccc agaagaaaat 360 372 qacctatttt aa <210> 80 <211> 123 <212> PRT <213> Streptococcus pneumoniae <400> 80 Met Ile Phe Asn Pro Ile Cys Cys Met Ile Arg Glu Lys Lys Gly Asp 10

Arg Asp Met Ala Phe Thr Asn Thr His Met Arg Ser Ala Ser Phe Gly

20 25 30

Ile Val Thr Ser Leu Pro Asp Asp Ile Ile Asp Ser Phe Trp Tyr Ile

Ile Asp His Phe Leu Lys Asn Val Phe Glu Leu Glu Glu Glu Leu Glu 50 55 60

Phe Gln Leu Leu Asn Asn Gln Gly Lys Ile Thr Phe His Phe Ser Ser 65 70 75 80

Gln His Leu Pro Thr Ala Ile Asp Phe Asp Phe Asn His Pro Phe Asp 85 90 95

Pro Arg Tyr Pro Pro Arg Val Leu Val Leu Asp Met Asp Gly Arg Glu 100 105 110

Thr Ile Leu Leu Pro Glu Glu Asn Asp Leu Phe 115 120

<210> 81

<211> 1645

<212> DNA

<213> Streptococcus pneumoniae

<400> 81

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<210> 82

<211> 548

<212> PRT

<213> Streptococcus pneumoniae

<400> 82

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Lys Ile Val Lys Lys Leu Glu Val Leu Met Lys Tyr Phe Val Pro Asn 20 25 30

Glu Val Phe Ser Ile Arg Lys Leu Lys Val Gly Thr Cys Ser Val Leu 35 40 45

Leu Ala Ile Ser Ile Leu Gly Ser Gln Gly Ile Leu Ser Asp Glu Val
50 55 60

Val Thr Ser Ser Ser Pro Met Ala Thr Lys Glu Ser Ser Asn Ala Ile 65 70 75 80

Thr Asn Asp Leu Asp Asn Ser Pro Thr Val Asn Gln Asn Arg Ser Ala 85 90 95

Glu Met Ile Ala Ser Asn Ser Thr Thr Asn Gly Leu Asp Asn Ser Leu 100 105 110

Ser Val Asn Ser Ile Ser Ser Asn Gly Thr Ile Arg Ser Asn Ser Gln 115 120 125

Leu Asp Asn Arg Thr Val Glu Ser Thr Val Thr Ser Thr Asn Glu Asn 130 135 140

Lys Ser Tyr Lys Glu Asp Val Ile Ser Asp Arg Ile Ile Lys Lys Glu 145 150 155 160

Phe Glu Asp Thr Ala Leu Ser Val Lys Asp Tyr Gly Ala Val Gly Asp 165 170 175

Gly Ile His Asp Asp Arg Gln Ala Ile Gln Asp Ala Ile Asp Ala Ala 180 185 190

Ala Gln Gly Leu Gly Gly Gly Asn Val Tyr Phe Pro Glu Gly Thr Tyr 195 200 205

Leu Val Lys Glu Ile Val Phe Leu Lys Ser His Thr His Leu Glu Leu 210 215 220

Asn Glu Lys Ala Thr Ile Leu Asn Gly Ile Asn Ile Lys Asn His Pro 225 230 235 240

Ser Ile Val Phe Met Thr Gly Leu Phe Thr Asp Asp Gly Ala Gln Val 245 250 255

Glu Trp Gly Pro Thr Glu Asp Ile Ser Tyr Ser Gly Gly Thr Ile Asp 260 265 270 Met Asn Gly Ala Leu Asn Glu Glu Gly Thr Lys Ala Lys Asn Leu Pro 275 280 285

Leu Ile Asn Ser Ser Gly Ala Phe Ala Ile Gly Asn Ser Asn Asn Val 290 295 300

Thr Ile Lys Asn Val Thr Phe Lys Asp Ser Tyr Gln Gly His Ala Ile 305 310 315 320

Gln Ile Ala Gly Ser Lys Asn Val Leu Val Asp Asn Ser Arg Phe Leu 325 330 335

Gly Gln Ala Leu Pro Lys Thr Met Lys Asp Gly Gln Ile Ile Ser Lys 340 345 350

Glu Ser Ile Gln Ile Glu Pro Leu Thr Arg Lys Gly Phe Pro Tyr Ala 355 360 365

Leu Asn Asp Asp Gly Lys Lys Ser Glu Asn Val Thr Ile Gln Asn Ser 370 375 380

Tyr Phe Gly Lys Ser Asp Lys Ser Gly Glu Leu Val Thr Ala Ile Gly 385 390 395 400

Thr His Tyr Gln Thr Leu Ser Thr Gln Asn Pro Ser Asn Ile Lys Ile 405 410 415

Gln Asn Asn His Phe Asp Asn Met Met Tyr Ala Gly Val Arg Phe Thr 420 425 430

Gly Phe Thr Asp Val Leu Ile Lys Gly Asn Arg Phe Asp Lys Lys Val

Lys Gly Glu Ser Val His Tyr Arg Glu Ser Gly Ala Ala Leu Val Asn 450 455 460

Ala Tyr Ser Tyr Lys Asn Thr Lys Asp Leu Leu Asp Leu Asn Lys Gln 465 470 475 480

Val Val Ile Ala Glu Asn Ile Phe Asn Ile Ala Asp Pro Lys Thr Lys
485 490 495

Ala Ile Arg Val Ala Lys Asp Ser Ala Glu Cys Leu Gly Lys Val Ser 500 505 510

Asp Ile Thr Val Thr Lys Asn Val Ile Asn Asn Asn Ser Lys Glu Thr 515 520 525

Glu Gln Pro Asn Ile Glu Leu Leu Arg Val Ser Asp Asn Leu Val Val
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Ser Glu Asn Ser 545

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816

Val Val Gly Ser Leu Leu Arg Tyr Tyr Glu Trp Met Gly Ile Ser Asn

230 235 240

Val Phe Leu Thr Lys Val Ile Pro Leu Ala Val Leu Phe Ile Gly Ile 245 250 255

Phe Val Leu Phe Arg Gly Phe Lys Lys Ile Lys Trp Ser Glu Val 260 265 270

<210> 87

225

<211> 348

<212> DNA

<213> Streptococcus pneumoniae

<400> 87

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<210> 88

<211> 115

<212> PRT

<213> Streptococcus pneumoniae

<400> 88

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Leu Ala Ala Gly Cys Ser Lys His Cys Phe Glu Val Val Asp Glu Thr 20 25 30

Asp Glu Val Ser Ser Lys His Val Phe Glu Val Val Asp Glu Thr Asp 35 40 45

Glu Val Ser Ser Lys His Cys Phe Glu Val Val Asp Glu Thr Asp Glu 50 55 60

Val Ser Ser Lys His Cys Phe Glu Val Val Asp Glu Thr Asp Glu Val 65 70 75 80

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Glu Glu Tyr 115

<210> 89

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<211> 1260

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Lys Asn Glu Ile Ile Ala Gly Arg Ser Leu Arg Glu Gln Asp Phe Lys 145 150 155 160

Glu Phe Ala Ser Val Ile Leu Leu Asp Glu Glu Leu Ser Ile Ser Leu 165 170 175

Phe Glu Ser Pro Gln Glu Ala Ile Asn Lys Val Val Glu Val Asn Gly 180 185 190

Phe Ser Tyr Arg Val Ile Gly Val Tyr Thr Ser Pro Glu Ala Lys Arg 195 200 205

Ser Lys Ile Tyr Gly Phe Gly Gly Leu Pro Ile Thr Thr Asn Ile Ser 210 215 220

Leu Ala Ala Asn Phe Asn Val Asp Glu Ile Ala Asn Ile Val Phe Arg 225 230 235 240

Val Asn Asp Thr Ser Leu Thr Pro Thr Leu Gly Pro Glu Leu Ala Arg 245 250 255

Lys Met Thr Glu Leu Ala Gly Leu Gln Gln Gly Glu Tyr Gln Val Ala 260 265 270

Asp Glu Ser Val Val Phe Ala Glu Ile Gln Gln Ser Phe Ser Phe Met 275 280 285

Thr Thr Ile Ile Ser Ser Ile Ala Gly Ile Ser Leu Phe Val Gly Gly 290 295 300

Thr Gly Val Met Asn Ile Met Leu Val Ser Val Thr Glu Arg Thr Arg 305 310 315 320

Glu Ile Gly Leu Arg Lys Ala Leu Gly Ala Thr Arg Ala Asn Ile Leu 325 330 335

Ile Gln Phe Leu Ile Glu Ser Met Ile Leu Thr Leu Leu Gly Gly Leu 340 345 350

Ile Gly Leu Thr Ile Ala Ser Gly Leu Thr Ala Leu Ala Gly Leu Leu 355 360 365

Leu Gln Gly Leu Ile Glu Gly Ile Glu Val Gly Val Ser Ile Pro Val 370 380

Ala Leu Phe Ser Leu Ala Val Ser Ala Ser Val Gly Met Ile Phe Gly 385 390 395

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Arg Tyr Glu

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705

<210> 91

145 150 155 160

Val Asn Asn Pro Ser Ile Ile Leu Ala Asp Glu Pro Thr Gly Ala Leu 165 170 175

Asp Thr Lys Thr Gly Asn Gln Ile Met Gln Leu Leu Val Asp Leu Asn 180 185 190

Lys Glu Gly Lys Thr Ile Ile Met Val Thr His Glu Pro Glu Ile Ala 195 200 205

Ala Tyr Ala Lys Arg Gln Ile Val Ile Arg Asp Gly Val Ile Ser Ser 210 215 220

Asp Ser Ala Gln Leu Gly Lys Glu Glu Asn 225 230

<210> 93

<211> 1200

<212> DNA

<213> Streptococcus pneumoniae

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<210> 94

<211> 399

<212> PRT

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Gly Gln Ala Leu Val Lys Tyr Ser Ser Ser Glu Ala Gln Ala Ala Tyr 100 105 110

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Leu Asn Gln Ala Arg Asn Glu Ala Ala Ser Ala Pro Ala Pro Gln Leu 130 135 140

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Val Ala Gly Asn Ser Val Ala Ser Ile Asp Ala Gln Leu Gly Asp Ala 165 170 175

Arg Asp Ala Arg Ala Asp Ala Ala Gln Leu Ser Lys Ala Gln Ser 180 185 190

Gln Leu Asp Ala Thr Thr Val Leu Ser Thr Leu Glu Gly Thr Val Val 195 200 205

Glu Val Asn Ser Asn Val Ser Lys Ser Pro Thr Gly Ala Ser Gln Val 210 215 220

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Ile Ser Asp Tyr Pro Lys Asn Asn Gly Glu Ala Ala Ser Pro Ala Ala 275 280 285

Gly Asn Asn Thr Gly Ser Lys Tyr Pro Tyr Thr Ile Asp Val Thr Gly 290 295 300

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Thr Thr Val Leu Ala Val Ala Lys Gly Ser Asn Leu Lys Val Ala Ala 50 55 60

Gln Asn Cys Tyr Phe Glu Asn Ala Gly Ala Phe Thr Gly Glu Thr Ser 65 70 75 80 Pro Gln Val Leu Lys Glu Ile Gly Thr Asp Tyr Val Val Ile Gly His 90 85 Ser Glu Arg Arg Asp Tyr Phe His Glu Thr Asp Glu Asp Ile Asn Lys 105 100 Lys Ala Lys Ala Ile Phe Ala Asn Gly Met Leu Pro Ile Ile Cys Cys 120 115 Gly Glu Ser Leu Glu Thr Tyr Glu Ala Gly Lys Ala Ala Glu Phe Val 135 Gly Ala Gln Val Ser Ala Ala Leu Ala Gly Leu Thr Ala Glu Gln Val 155 150 145 Ala Ala Ser Val Ile Ala Tyr Glu Pro Ile Trp Ala Ile Gly Thr Gly 170 Lys Ser Ala Ser Gln Asp Asp Ala Gln Lys Met Cys Lys Val Val Arg 190 185 Asp Val Val Ala Ala Asp Phe Gly Gln Glu Val Ala Asp Lys Val Arg 200 195 Val Gln Tyr Gly Gly Ser Val Lys Pro Glu Asn Val Ala Ser Tyr Met 215 Ala Cys Pro Asp Val Asp Gly Ala Leu Val Gly Gly Ala Ser Leu Glu 230 235 225 Ala Glu Ser Phe Leu Ala Leu Leu Asp Phe Val Lys 245 250

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Lys Thr Gln Thr Ser Ala Glu Val Gln Thr Asn Ala Ala Ala His Trp

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Trp Ile Phe Asp Asn Tyr Tyr Lys Ala Trp Phe Tyr Ile Asn Ser Asp

Gly Arg Tyr Ser Gln Asn Glu Trp His Gly Asn Tyr Tyr Leu Lys Ser 105 100

Gly Gly Tyr Met Ala Gln Asn Glu Trp Ile Tyr Asp Ser Asn Tyr Lys 125 115

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Ala Lys Ser Gln Trp Gln Gly Ser Tyr Phe Leu Asn Gly Gln Gly Ala 170 165

Met Met Gln Asn Glu Trp Leu Tyr Asp Pro Ala Tyr Ser Ala Tyr Phe 185

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Glu Trp Gln Gly Asn Tyr Tyr Leu Thr Gly Ser Gly Ala Met Ala Thr 225 230 235 240

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His Ala Lys Lys Val Ile Asp Ile Ser Glu His Asn Gly Arg Ile Asn 290 295 300

Asp Trp Lys Lys Val Ile Asp Glu Asn Glu Val Asp Gly Val Ile Val 305 310 315 320

Arg Leu Gly Tyr Ser Gly Lys Glu Asp Lys Glu Leu Ala His Asn Ile 325 330 335

Lys Glu Leu Asn Arg Leu Gly Ile Pro Tyr Gly Val Tyr Leu Tyr Thr 340 345 350

Tyr Ala Glu Asn Glu Thr Asp Ala Glu Ser Asp Ala Lys Gln Thr Ile 355 360 365

Glu Leu Ile Lys Lys Tyr Asn Met Asn Leu Ser Tyr Pro Ile Tyr Tyr 370 375 380

Asp Val Glu Asn Trp Glu Tyr Val Asn Lys Ser Lys Arg Ala Pro Ser 385 390 395 400

Asp Thr Gly Thr Trp Val Lys Ile Ile Asn Lys Tyr Met Asp Thr Met 405 410 415

Lys Gln Ala Gly Tyr Gln Asn Val Tyr Val Tyr Ser Tyr Arg Ser Leu 420 425 430

Leu Gln Thr Arg Leu Lys His Pro Asp Ile Leu Lys His Val Asn Trp
435 440 445

Val Ala Ala Tyr Thr Asn Ala Leu Glu Trp Glu Asn Pro His Tyr Ser 450 455 460

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120

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Val Leu Pro Arg Leu Lys Glu Met Asn Gly Asp Met Ile His Ala Ala 155 150

Tyr Asp Leu Gly Ala Ser Gln Phe Gln Met Phe Lys Glu Ile Met Leu

165 170 175

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- Glu Leu Leu Thr Gln Phe Thr Glu Glu Thr Gly Ile Gln Val Gln Tyr 50 55 60
- Glu Thr Phe Asp Ser Asn Glu Ala Met Tyr Thr Lys Ile Lys Gln Gly
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- Gly Thr Thr Tyr Asp Ile Ala Ile Pro Ser Glu Tyr Met Ile Asn Lys 85 90 95
- Met Lys Asp Glu Asp Leu Leu Val Pro Leu Asp Tyr Ser Lys Ile Glu 100 105 110
- Gly Ile Glu Asn Ile Gly Pro Glu Phe Leu Asn Gln Ser Phe Asp Pro 115 120 125
- Gly Asn Lys Phe Ser Ile Pro Tyr Phe Trp Gly Thr Leu Gly Ile Val 130 135 140
- Tyr Asn Glu Thr Met Val Asp Glu Ala Pro Glu His Trp Asp Asp Leu 145 150 155 160
- Trp Lys Pro Glu Tyr Lys Asn Ser Ile Met Leu Phe Asp Gly Ala Arg 165 170 175
- Glu Val Leu Gly Leu Gly Leu Asn Ser Leu Gly Tyr Ser Leu Asn Ser 180 185 190
- Lys Asp Leu Gln Gln Leu Glu Glu Thr Val Asp Lys Leu Tyr Lys Leu 195 200 205
- Thr Pro Asn Ile Lys Ala Ile Val Ala Asp Glu Met Lys Gly Tyr Met 210 215 220
- Ile Gln Asn Asn Val Ala Ile Gly Val Thr Phe Ser Gly Glu Ala Ser 225 230 235 240
- Gln Met Leu Glu Lys Asn Glu Asn Leu Arg Tyr Val Val Pro Thr Glu 245 250 255
- Ala Ser Asn Leu Trp Phe Asp Asn Met Val Ile Pro Lys Thr Val Lys 260 265 270
- Asn Gln Asn Ser Ala Tyr Ala Phe Ile Asn Phe Met Leu Lys Pro Glu 275 280 285
- Asn Ala Leu Gln Asn Ala Glu Tyr Val Gly Tyr Ser Thr Pro Asn Leu 290 295 300
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Met Val Val Ser Ile Ile Val Ser Tyr Ile Leu Phe Tyr Gly Leu Ile 35 40 45

Asn Pro Ala Pro Val Asp Tyr Ile Ile Tyr Thr Ser Leu Ala Phe Leu 50 55 60

Phe Tyr Gln Leu Met Ile Gly Phe Trp Gly Leu Asn Ala Ser Ile Ser 65 70 75 80

Arg Tyr Ser Lys Ile Thr Asp Phe Met Lys Ile Phe Phe Gly Val Thr 85 90 95

Ala Ser Ser Val Leu Ser Tyr Ser Ile Cys Tyr Ala Phe Leu Pro Leu 100 105 110

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Ile Leu Leu Pro Arg Ile Thr Trp Gln Leu Ile Tyr Ser Arg Arg Lys 130 135 140

Lys Gly Ser Gly Asp Gly Glu His Arg Arg Thr Phe Leu Ile Gly Ala 145 150 155 160

Gly Asp Gly Gly Ala Leu Phe Met Asp Ser Tyr Gln His Pro Thr Ser 165 170 175

Glu Leu Glu Leu Val Gly Ile Leu Asp Lys Asp Ser Lys Lys Gly 180 185 190

Gln Lys Leu Gly Gly Ile Pro Val Leu Gly Ser Tyr Asp Asn Leu Pro 195 200 205

Glu Leu Ala Lys Arg His Gln Ile Glu Arg Val Ile Val Ala Ile Pro 210 215 220

Ser Leu Asp Pro Ser Glu Tyr Glu Arg Ile Leu Gln Met Cys Asn Lys 225 230 235 240

Leu Gly Val Lys Cys Tyr Lys Met Pro Lys Val Glu Thr Val Val Gln 245 250 255

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Leu Leu Gly Arg Gln Glu Ile Arg Leu Asp Glu Ser Arg Leu Gly Ala 275 280 285

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Val Leu Leu Gly His Gly Glu Asn Ser Ile Tyr Leu Val Tyr His Glu 325 330 335

305

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Ile Gln Asp Tyr Asp Arg Leu Leu Gln Val Phe Glu Gln Tyr Lys Pro 355 360 365

Ala Ile Val Tyr His Ala Ala Ala His Lys His Val Pro Met Met Glu 370 380

Arg Asn Pro Lys Glu Ala Phe Lys Asn Asn Ile Arg Gly Thr Tyr Asn 385 390 395 400

Val Ala Lys Ala Val Asp Glu Ala Lys Val Ser Lys Met Val Met Ile 405 410 415

Ser Thr Asp Lys Ala Val Asn Pro Pro Asn Val Met Gly Ala Thr Lys 420 425 430

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Thr Tyr Cys Ala Val Arg Phe Gly Asn Val Leu Gly Ser Arg Gly Ser 450 455 460

Val Ile Pro Val Phe Glu Arg Gln Ile Ala Glu Gly Gly Pro Val Thr 465 470 475 480

Val Thr Asp Phe Arg Met Thr Arg Tyr Phe Met Thr Ile Pro Glu Ala 485 490 495

Ser Arg Leu Val Ile His Ala Gly Ala Tyr Ala Lys Asp Gly Glu Val 500 505 510

Phe Ile Leu Asp Met Gly Lys Pro Val Lys Ile Tyr Asp Leu Ala Lys 515 520 525

Lys Met Val Leu Leu Ser Gly His Thr Glu Ser Glu Ile Pro Ile Val 530 535 540

Glu Val Gly Ile Arg Pro Gly Glu Lys Leu Tyr Glu Glu Leu Leu Val 545 550 555 560

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Ala Asp Gly Phe Leu Pro Asp Gly Leu Leu Ser Pro Phe Thr Tyr Tyr
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Leu Gly Tyr Glu Asp Gly Lys Pro Leu Tyr Phe Asn Gln Val Pro Val
Ser Asp Phe Trp Glu Ile Leu Gly Asp Asn Gln Ser Ala Cys Ile Glu
 Asp Val Thr Gln Glu Arg Ala Val Ile His Tyr Ala Asp Gly Met Gln
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1338

85 90 95

Ala Arg Leu Val Lys Gln Val Asp Trp Lys Asp Leu Glu Gly Arg Val 100 105 110

Arg Gln Val Asp His Tyr Asn Arg Phe Gly Ala Cys Phe Ala Thr Thr 115 120 125

Thr Tyr Ser Ala Asp Ser Glu Pro Ile Met Thr Val Tyr Gln Asp Val 130 135 140

Asn Gly Gln Gln Val Leu Leu Glu Asn His Val Thr Gly Asp Ile Leu 145 150 155 160

Leu Thr Leu Pro Gly Gln Ser Met Arg Tyr Phe Ala Asn Lys Val Glu 165 170 175

Phe Ile Thr Phe Phe Leu Gln Asp Leu Glu Ile Asp Thr Ser Gln Leu 180 185 190

Ile Phe Asn Thr Leu Ala Thr Pro Phe Leu Val Ser Phe His His Pro 195 200 205

Asp Lys Ser Gly Ser Asp Val Leu Val Trp Gln Glu Pro Leu Tyr Asp 210 215 220

Ala Ile Pro Gly Asn Met Gln Leu Ile Leu Glu Ser Asp Asn Val Arg 225 230 235 240

Thr Lys Lys Ile Ile Ile Pro Asn Lys Ala Thr Tyr Glu Arg Ala Leu 245 250 255

Glu Leu Thr Asp Glu Lys Tyr His Asp Gln Phe Val His Leu Gly Tyr 260 265 270

His Tyr Gln Phe Lys Arg Asp Asn Phe Leu Arg Arg Asp Ala Leu Ile 275 280 285

Leu Thr Asn Ser Asp Gln Ile Glu Gln Val Glu Ala Ile Ala Gly Ala 290 295 300

Leu Pro Asp Val Thr Phe Arg Ile Ala Ala Val Thr Glu Met Ser Ser 305 310 315 320

Lys Leu Leu Asp Met Leu Cys Tyr Pro Asn Val Ala Leu Tyr Gln Asn 325 330 335

Ala Ser Pro Gln Lys Ile Gln Glu Leu Tyr Gln Leu Ser Asp Ile Tyr 340 345 350

Leu Asp Ile Asn His Ser Asn Glu Leu Leu Gln Ala Val Arg Gln Ala 355 360 365

Phe Glu His Asn Leu Leu Ile Leu Gly Phe Asn Gln Thr Val His Asn 370 380

Arg Leu Tyr Ile Ala Pro Asp His Leu Phe Glu Ser Ser Glu Val Ala

385 390 395 400

Ala Leu Val Glu Thr Ile Lys Leu Ala Leu Ser Asp Val Asp Gln Met 405 410 415

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<210> 108 <211> 503

<212> PRT

<213> Streptococcus pneumoniae

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Val Glu Tyr Ala Gln Ala Tyr Arg Ala Gly Val Phe Arg Lys Leu Asn

20 25 30

Leu Ser Ser Lys Phe Ile Phe Thr Asp Met Ile Leu Ala Asp Asn Ile 35 40 45

- Gln His Leu Thr Ala Asn Ile Gly Phe Asp Asp Asn Gln Val Ile Trp
 50 55 60
- Leu Tyr Asn His Phe Thr Asp Ile Lys Ile Ala Pro Thr Ser Val Thr 65 70 75 80
- Val Asp Asp Val Leu Ala Tyr Phe Gly Gly Glu Glu Ser His Arg Glu 85 90 95
- Lys Asn Gly Lys Val Leu Arg Val Phe Phe Phe Asp Gln Asp Lys Phe 100 105 110
- Val Thr Cys Tyr Leu Val Asp Glu Asn Lys Asp Leu Val Gln His Ala 115 120 125
- Glu Tyr Val Phe Lys Gly Asn Leu Ile Arg Lys Asp Tyr Phe Ser Tyr 130 135 140
- Thr Arg Tyr Cys Ser Glu Tyr Phe Ala Pro Lys Asp Asn Val Ala Val 145 150 155 160
- Leu Tyr Gln Arg Thr Phe Tyr Asn Glu Asp Gly Thr Pro Val Tyr Asp 165 170 175
- Ile Leu Met Asn Gln Gly Lys Glu Glu Val Tyr His Phe Lys Asp Lys 180 185 190
- Ile Phe Tyr Gly Lys Gln Ala Phe Val Arg Ala Phe Met Lys Ser Leu
- Asn Leu Asn Lys Ser Asp Leu Val Ile Leu Asp Arg Glu Thr Gly Ile 210 215 220
- Gly Gln Val Val Phe Glu Glu Ala Gln Thr Ala His Leu Ala Val Val 225 230 235 240
- Val His Ala Glu His Tyr Ser Glu Asn Ala Thr Asn Glu Asp Tyr Ile 245 250 255
- Leu Trp Asn Asn Tyr Tyr Asp Tyr Gln Phe Thr Asn Ala Asp Lys Val 260 265 270
- Asp Phe Phe Ile Val Ser Thr Asp Arg Gln Asn Glu Val Leu Gln Glu 275 280 285
- Gln Phe Ala Lys Tyr Thr Gln His Gln Pro Lys Ile Val Thr Ile Pro 290 295 300
- Val Gly Ser Ile Asp Ser Leu Thr Asp Ser Ser Gln Gly Arg Lys Pro 305 310 315 320
- Phe Ser Leu Ile Thr Ala Ser Arg Leu Ala Lys Glu Lys His Ile Asp

325 330 335

Trp Leu Val Lys Ala Val Ile Glu Ala His Lys Glu Leu Pro Glu Leu 340 345 350

Thr Phe Asp Ile Tyr Gly Ser Gly Gly Glu Asp Ser Leu Leu Arg Glu 355 360 365

Ile Ile Ala Asn His Gln Ala Glu Asp Tyr Ile Gln Leu Lys Gly His 370 375 380

Ala Glu Leu Ser Gln Ile Tyr Ser Gln Tyr Glu Val Tyr Leu Thr Ala 385 390 395 400

Ser Thr Ser Glu Gly Phe Gly Leu Thr Leu Met Glu Ala Ile Gly Ser 405 410 415

Gly Leu Pro Leu Ile Gly Phe Asp Val Pro Tyr Gly Asn Gln Thr Phe 420 425 430

Ile Glu Asp Gly Gln Asn Gly Tyr Leu Ile Pro Ser Ser Asp His 435 440 445

Val Glu Asp Gln Ile Lys Gln Ala Tyr Ala Ala Lys Ile Cys Gln Leu 450 455 460

Tyr Gln Glu Asn Arg Leu Glu Ala Met Arg Ala Tyr Ser Tyr Gln Ile 465 470 475 480

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Val Glu Glu Val Leu His Asp 500

<210> 109

<211> 2292

<212> DNA

<213> Streptococcus pneumoniae

<400> 109

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<210> 110 <211> 763

<212> PRT

<213> Streptococcus pneumoniae

<400> 110

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Ala Phe Ala Val Val Arg Glu Ala Asp Lys Arg Ile Leu Gly Met Phe 35 40 45

Pro Tyr Asp Val Gln Val Met Gly Ala Ile Val Met His Tyr Gly Asn 50 55 60

Val Ala Glu Met Asn Thr Gly Glu Gly Lys Thr Leu Thr Ala Thr Met
65 70 75 80

Pro Val Tyr Leu Asn Ala Phe Ser Gly Glu Gly Val Met Val Val Thr 85 90 95

Pro Asn Glu Tyr Leu Ser Lys Arg Asp Ala Glu Glu Met Gly Gln Val

Tyr Arg Phe Leu Gly Leu Thr Ile Gly Val Pro Phe Thr Glu Asp Pro 115 120 125 Lys Lys Glu Met Lys Ala Glu Glu Lys Lys Leu Ile Tyr Ala Ser Asp 135 130 Ile Ile Tyr Thr Thr Asn Ser Asn Leu Gly Phe Asp Tyr Leu Asn Asp 150 Asn Leu Ala Ser Asn Glu Glu Gly Lys Phe Leu Arg Pro Phe Asn Tyr 170 Val Ile Ile Asp Glu Ile Asp Asp Ile Leu Leu Asp Ser Ala Gln Thr 185 Pro Leu Ile Ile Ala Gly Ser Pro Arg Val Gln Ser Asn Tyr Tyr Ala 200 Ile Ile Asp Thr Leu Val Thr Leu Val Glu Gly Glu Asp Tyr Ile 215 Phe Lys Glu Glu Lys Glu Glu Val Trp Leu Thr Thr Lys Gly Ala Lys 235 230 Ser Ala Glu Asn Phe Leu Gly Ile Asp Asn Leu Tyr Lys Glu Glu His 250 245 Ala Ser Phe Ala Arg His Leu Val Tyr Ala Ile Arg Ala His Lys Leu 265 260 Phe Thr Lys Asp Lys Asp Tyr Ile Ile Arg Gly Asn Glu Met Val Leu 280 Val Asp Lys Gly Thr Gly Arg Leu Met Glu Met Thr Lys Leu Gln Gly 295 Gly Leu His Gln Ala Ile Glu Ala Lys Glu His Val Lys Leu Ser Pro 310 305 Glu Thr Arg Ala Met Ala Ser Ile Thr Tyr Gln Ser Leu Phe Lys Met 330 325 Phe Asn Lys Ile Ser Gly Met Thr Gly Thr Gly Lys Val Ala Glu Lys 340 Glu Phe Ile Glu Thr Tyr Asn Met Ser Val Val Arg Ile Pro Thr Asn Arg Pro Arg Gln Arg Ile Asp Tyr Pro Asp Asn Leu Tyr Ile Thr Leu 375 Pro Glu Lys Val Tyr Ala Ser Leu Glu Tyr Ile Lys Gln Tyr His Ala 390 385 Lys Gly Asn Pro Leu Leu Val Phe Val Gly Ser Val Glu Met Ser Gln 410 Leu Tyr Ser Ser Leu Leu Phe Arg Glu Gly Ile Ala His Asn Val Leu

430

425

420

- Asn Ala Asn Asn Ala Ala Arg Glu Ala Gln Ile Ile Ser Glu Ser Gly
 435
 440
 445
- Gln Met Gly Ala Val Thr Val Ala Thr Ser Met Ala Gly Arg Gly Thr 450 455 460
- Asp Ile Lys Leu Gly Lys Gly Val Ala Glu Leu Gly Gly Leu Ile Val 465 470 475 480
- Ile Gly Thr Glu Arg Met Glu Ser Gln Arg Ile Asp Leu Gln Ile Arg 485 490 495
- Gly Arg Ser Gly Arg Gln Gly Asp Pro Gly Met Ser Lys Phe Phe Val
- Ser Leu Glu Asp Asp Val Ile Lys Lys Phe Gly Pro Ser Trp Val His 515 520 525
- Lys Lys Tyr Lys Asp Tyr Gln Val Gln Asp Met Thr Gln Pro Glu Val 530 535 540
- Leu Lys Gly Arg Lys Tyr Arg Lys Leu Val Glu Lys Ala Gln His Ala 545 550 555
- Ser Asp Ser Ala Gly Arg Ser Ala Arg Arg Gln Thr Leu Glu Tyr Ala 565 570 575
- Glu Ser Met Asn Ile Gln Arg Asp Ile Val Tyr Lys Glu Arg Asn Arg 580 585 590
- Leu Ile Asp Gly Ser Arg Asp Leu Glu Asp Val Val Asp Ile Ile 595 600 605
- Glu Arg Tyr Thr Glu Glu Val Ala Ala Asp His Tyr Ala Ser Arg Glu
- Leu Leu Phe His Phe Ile Val Thr Asn Ile Ser Phe His Val Lys Glu 625 630 635 640
- Val Pro Asp Tyr Ile Asp Val Thr Asp Lys Thr Ala Val Arg Ser Phe 645 650 655
- Met Lys Gln Val Ile Asp Lys Glu Leu Ser Glu Lys Lys Glu Leu Leu 660 665 670
- Asn Gln His Asp Leu Tyr Glu Gln Phe Leu Arg Leu Ser Leu Leu Lys 675 680 685
- Ala Ile Asp Asp Asn Trp Val Glu Gln Val Asp Tyr Leu Gln Gln Leu 690 695 700
- Ser Met Ala Ile Gly Gly Gln Ser Ala Ser Gln Lys Asn Pro Ile Val 705 710 715 720
- Glu Tyr Tyr Gln Glu Ala Tyr Ala Gly Phe Glu Ala Met Lys Glu Gln 725 730 735

Ile His Ala Asp Met Val Arg Asn Leu Leu Met Gly Leu Val Glu Val 745 740 Thr Pro Lys Gly Glu Ile Val Thr His Phe Pro 760 755 <210> 111 <211> 879 <212> DNA <213> Streptococcus pneumoniae <400> 111 atgaaacaag aatggtttga aagtaatgat tttgtaaaaa caacaagcaa gaacaagcct 60 gaagagcaag ctcaagaggt tgcagacaag gctgaagaaa ggatacccga tctcgataca 120 ccaattgaaa aaaatactca gttagaggag gaagtctctc aagctgaagt cgaattggaa 180 agccagcaag aagagaaaat tgaagctcct gaagacagtg aagcgagaac agaaatagaa 240 gaaaagaagg catctaattc tactgaagaa gagccagacc tttctaaaga aacagaaaaa 300 gtcactatag ctgaagagag ccaagaagct cttcctcagc aaaaagcaac cacgaaagag 360 ccacttetta teagtaaate tttagaaagt cettatatee eegaceaage teeaaaatet 420 agggataaat ggaaagagca agtgcttgat ttttggtctt ggctagtgga agcgatcaaa 480 tetectacaa gtaagttgga aacaagtate acacaggtt acacageett tetettgete 540 attctgtttt ctgcatcttc ctttttcttt agtatctatc acatcaaaca tgcttactat 600 ggacatatag caagcattaa cagtcgcttc cctgagcagc tagctccttt aactcttttt 660 totatcatet ctatectagt agegacaaca etettettet ttteatteet ettgggtagt 720 ttcgttgtga gacgatttat ccaccaggaa aaggactgga cgctagacaa ggttctccaa 780 caatatagtc aactettggc aattecaate teetcactgc tattgctagt ttetttgctt 840 879 tctttgatag cctacgattt acagccctct tgtgtgtga <210> 112 <211> 292 <212> PRT <213> Streptococcus pneumoniae <400> 112 Met Lys Gln Glu Trp Phe Glu Ser Asn Asp Phe Val Lys Thr Thr Ser 10 5 Lys Asn Lys Pro Glu Glu Gln Ala Gln Glu Val Ala Asp Lys Ala Glu 25 Glu Arg Ile Pro Asp Leu Asp Thr Pro Ile Glu Lys Asn Thr Gln Leu 40 45 35 Glu Glu Glu Val Ser Gln Ala Glu Val Glu Leu Glu Ser Gln Gln Glu 50 Glu Lys Ile Glu Ala Pro Glu Asp Ser Glu Ala Arg Thr Glu Ile Glu 75 Glu Lys Lys Ala Ser Asn Ser Thr Glu Glu Glu Pro Asp Leu Ser Lys 90

Glu Thr Glu Lys Val Thr Ile Ala Glu Glu Ser Gln Glu Ala Leu Pro 105

100

Gln Gln Lys Ala Thr Thr Lys Glu Pro Leu Leu Ile Ser Lys Ser Leu 115 Glu Ser Pro Tyr Ile Pro Asp Gln Ala Pro Lys Ser Arg Asp Lys Trp 135 Lys Glu Gln Val Leu Asp Phe Trp Ser Trp Leu Val Glu Ala Ile Lys 150 Ser Pro Thr Ser Lys Leu Glu Thr Ser Ile Thr His Ser Tyr Thr Ala 170 Phe Leu Leu Ile Leu Phe Ser Ala Ser Ser Phe Phe Ser Ile 185 180 Tyr His Ile Lys His Ala Tyr Tyr Gly His Ile Ala Ser Ile Asn Ser 200 Arg Phe Pro Glu Gln Leu Ala Pro Leu Thr Leu Phe Ser Ile Ile Ser 220 215 Ile Leu Val Ala Thr Thr Leu Phe Phe Phe Ser Phe Leu Leu Gly Ser 235 230 225 Phe Val Val Arg Arg Phe Ile His Gln Glu Lys Asp Trp Thr Leu Asp 250 245 Lys Val Leu Gln Gln Tyr Ser Gln Leu Leu Ala Ile Pro Ile Ser Ser 265 260 Leu Leu Leu Val Ser Leu Leu Ser Leu Ile Ala Tyr Asp Leu Gln 280 275 Pro Ser Cys Val 290 <210> 113 <211> 327 <212> DNA <213> Streptococcus pneumoniae <400> 113 atgtactttc caacatcctc tgccttgatt gaatttctca tcttggctgt actggagcag 60 ggtgattett atggttatga gattagecaa accattaage tgategetaa tateaaagaa 120 tecacaetet ateceattet caaaaaattg gaaggeaata getttetgae aacetattet 180 agagagttcc aaggtcgcat gcgcaaatac tactccttga caaacggtgg tatagagcag 240 ctcttgaccc taaaagatga atgggcactc tatacagaca ccatcaatgg catcatagaa 300 1327 gggagtatcc gccatgacaa gaactga <210> 114 <211> 108 <212> PRT <213> Streptococcus pneumoniae

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                  5
Val Leu Glu Gln Gly Asp Ser Tyr Gly Tyr Glu Ile Ser Gln Thr Ile
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Lys Leu Ile Ala Asn Ile Lys Glu Ser Thr Leu Tyr Pro Ile Leu Lys
                             40
Lys Leu Glu Gly Asn Ser Phe Leu Thr Thr Tyr Ser Arg Glu Phe Gln
     50
Gly Arg Met Arg Lys Tyr Tyr Ser Leu Thr Asn Gly Gly Ile Glu Gln
Leu Leu Thr Leu Lys Asp Glu Trp Ala Leu Tyr Thr Asp Thr Ile Asn
                                      90
Gly Ile Ile Glu Gly Ser Ile Arg His Asp Lys Asn
                                 105
            100
<210> 115
 <211> 954
 <212> DNA
 <213> Streptococcus pneumoniae
 <400> 115
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 qatggtgaaa ctgagctaaa ccaggtcaaa gacaacaatc aggcccttaa gcgtttagca 180
 ctacgcaaag aagaatggct caagacctac cagtttctct tgatgaaggc tgggcaaaca 240
 gaaccettge aggecaatea ceagtttaca eeggatgeta tigetttget titggtgttt 300
 attgtggaag agttgtttaa agaggaggaa attactatcc tcgaaatggg ttctgggatg 360
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 gctggctttg tccaaggaga tgccgttcgc ccacaaatgc tcaaagaaag cgatgtggtc 540
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 gettetagee aagaacatae ttacgeecat caettgetea tggaacaagg gettaagtae 660
 ctcaagtcag acggatacgc tatttttcta gctccgagtg atttgttgac cagtcctcaa 720
 agtgatttgt taaaagaatg gctgaaagaa gaggcgagtc tggttgctat gattagtctg 780
 cctgaaaatc tctttgctaa tgccaaacaa tctaagacta tttttatctt acagaagaaa 840
 aatgaaatag cagtagagcc ttttgtttat ccacttgcta gcttgcaaga tgcaagtgtt 900
 ttaatgaaat ttaaagaaaa ttttcaaaaa tggactcaag gtactgaaat ataa
 <210> 116
 <211> 317
 <212> PRT
 <213> Streptococcus pneumoniae
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10

1

Val Gln Val Ile Gln Ser Asp Leu Ala Thr Asn Phe Tyr Asp Ala Leu 20 25 30

. .

- Val Glu Gln Asn Ser Ile Tyr Leu Asp Gly Glu Thr Glu Leu Asn Gln 35 40 45
- Val Lys Asp Asn Asn Gln Ala Leu Lys Arg Leu Ala Leu Arg Lys Glu
 50 55 60
- Glu Trp Leu Lys Thr Tyr Gln Phe Leu Leu Met Lys Ala Gly Gln Thr 65 70 75 80
- Glu Pro Leu Gln Ala Asn His Gln Phe Thr Pro Asp Ala Ile Ala Leu 85 90 95
- Leu Leu Val Phe Ile Val Glu Glu Leu Phe Lys Glu Glu Glu Ile Thr
- Ile Leu Glu Met Gly Ser Gly Met Gly Ile Leu Gly Ala Ile Phe Leu 115 120 125
- Thr Ser Leu Thr Lys Lys Val Asp Tyr Leu Gly Met Glu Val Asp Asp 130 135 140
- Leu Leu Ile Asp Leu Ala Ala Ser Met Ala Asp Val Ile Gly Leu Gln 145 150 155 160
- Ala Gly Phe Val Gln Gly Asp Ala Val Arg Pro Gln Met Leu Lys Glu 165 170 175
- Ser Asp Val Val Ile Ser Asp Leu Pro Val Gly Tyr Tyr Pro Asp Asp 180 185 190
- Ala Val Ala Ser Arg His Gln Val Ala Ser Ser Gln Glu His Thr Tyr
- Ala His His Leu Leu Met Glu Gln Gly Leu Lys Tyr Leu Lys Ser Asp 210 215 220
- Gly Tyr Ala Ile Phe Leu Ala Pro Ser Asp Leu Leu Thr Ser Pro Gln 225 230 235 240
- Ser Asp Leu Leu Lys Glu Trp Leu Lys Glu Glu Ala Ser Leu Val Ala 245 250 255
- Met Ile Ser Leu Pro Glu Asn Leu Phe Ala Asn Ala Lys Gln Ser Lys 260 265 270
- Thr Ile Phe Ile Leu Gln Lys Lys Asn Glu Ile Ala Val Glu Pro Phe 275 280 285
- Val Tyr Pro Leu Ala Ser Leu Gln Asp Ala Ser Val Leu Met Lys Phe 290 295 300
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325

340

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- Phe Gly Ala Asn Val Glu Val Gly Tyr Tyr Asp Gln Thr Gln Ser Lys 385 390 395 400
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- Leu Thr Pro Glu Val Glu Ile Arg Asn Arg Leu Gly Ala Phe Leu Phe 420 425 430
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- Lys Ala Arg Leu Leu Leu Ala Lys Leu Ser Met Glu Asn Asn Asn Phe 450 455 460
- Leu Ile Leu Asp Glu Pro Thr Asn His Leu Asp Ile Asp Ser Lys Glu 465 470 475 480
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- Ser His Asp Arg Tyr Phe Ile Asn Arg Val Ala Thr His Val Leu Glu
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- Leu Ser Glu Asn Gly Ser Thr Leu Tyr Leu Gly Asp Tyr Asp Tyr Tyr 515 520 525
- Val Glu Lys Lys Ala Thr Ala Glu Met Ser Gln Thr Glu Glu Ala Ser 530 540
- Thr Ser Asn Gln Ala Lys Glu Ala Ser Pro Val Asn Asp Tyr Gln Ala 545 550 555 560
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- Ser Leu Glu Ala Glu Ile Glu Glu Leu Glu Ser Gln Ser Gln Ala Ile 580 585 590
- Ser Glu Gln Met Leu Glu Thr Asn Asp Ala Asp Lys Leu Met Glu Leu 595 600 605
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120

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. . . .

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- Leu His Met Thr Leu Leu Leu Asp Ser Leu Thr Phe Phe Ile Ala Phe 165 170 175
- Val Leu Val Ala Phe Leu Pro Lys Glu Glu Ala Lys Val Gln Glu Lys 180 185 190
- Lys Ala Phe Thr Gly Arg Asp Ile Phe Val Asp Ile Lys Asp Gly Leu 195 200 205
- His Tyr Ile Trp His Gln Gln Glu Ile Phe Phe Leu Leu Val Ala 210 215 220
- Ser Ser Val Asn Phe Phe Phe Ala Ala Phe Glu Phe Leu Leu Pro Phe 225 230 235 240
- Ser Asn Gln Leu Tyr Gly Ser Glu Gly Ala Tyr Ala Ser Ile Leu Thr 245 250 255
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- Lys Ala Asn Ile Tyr Asn Leu Leu Ile Leu Leu Ala Leu Thr Gly Val 275 280 285
- Gly Val Phe Met Met Gly Leu Pro Leu Pro Thr Phe Leu Ser Phe Ser
- Gly Asn Leu Val Cys Glu Leu Phe Met Thr Ile Phe Asn Ile His Phe 305 310 315 320
- Phe Thr Gln Val Gln Thr Lys Val Glu Ser Glu Phe Leu Gly Arg Val 325 330 335
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- Gly Phe Met Thr Val Leu Pro Ser Val His Leu Tyr Ser Phe Leu Ile 355 360 365
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Gly Phe Leu Gly Gly Met Leu Gly Ala Gly Ile Ala Leu Gly Tyr Gly 65 70 75 80

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Asn Gln Val Lys Asp Ile Ser Ser Ile Ser Glu Ile Thr Tyr Ser Asp 100 105 110

Gly Thr Val Ile Ala Ser Ile Glu Ser Asp Leu Leu Arg Thr Ser Ile 115 120 125

Ser Ser Glu Gln Ile Ser Glu Asn Leu Lys Lys Ala Ile Ile Ala Thr 130 135 140

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Ile Arg Ala Thr Leu Gly Lys Phe Val Gly Leu Gly Ser Ser Gly 165 170 175

Gly Ser Thr Leu Thr Gln Gln Leu Ile Lys Gln Gln Val Val Gly Asp 180 185 190

Ala Pro Thr Leu Ala Arg Lys Ala Ala Glu Ile Val Asp Ala Leu Ala 195 200 205

Leu Glu Arg Ala Met Asn Lys Asp Glu Ile Leu Thr Thr Tyr Leu Asn 210 215 220

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Val Pro Gln Ala Ala Phe Leu Ala Gly Leu Pro Gln Ser Pro Ile Thr 260 265 270

Tyr Ser Pro Tyr Glu Asn Thr Gly Glu Leu Lys Ser Asp Glu Asp Leu 275 280 285

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Thr Gly Ala Leu Ser Lys Asp Glu Tyr Ser Gln Tyr Lys Asp Tyr Asp 305 310 315

Leu Lys Gln Asp Phe Leu Pro Ser Gly Thr Val Thr Gly Ile Ser Arg

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Ala Met Gln Ser Ala Val Ala Asp Tyr Gly Tyr Leu Leu Asp Asp Gly 405 410 415

Thr Gly Arg Val Glu Val Gly Asn Val Leu Met Asp Asn Gln Thr Gly 420 425 430

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Leu Asn Tyr Ser Trp Asn Ile Pro Ala Tyr Trp Thr Tyr Arg Met Leu 515 520 525

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Glu Ile Pro Glu Tyr Gly Ile Glu Ser Leu Pro Met Gly Gly Ile 545 550 555 560

Glu Val Thr Val Ala Gln His Thr Asn Gly Tyr Gln Thr Leu Ala Asn . 565 570 575

Asn Gly Val Tyr His Gln Lys His Val Ile Ser Lys Ile Glu Ala Ala 580 585 590

Asp Gly Arg Val Val Tyr Glu Tyr Gln Asp Lys Pro Val Gln Val Tyr 595 600 605

Ser Lys Ala Thr Ala Thr Ile Met Gln Gly Leu Leu Arg Glu Val Leu 610 620

Ser Ser Arg Val Thr Thr Thr Phe Lys Ser Asn Leu Thr Ser Leu Asn

625 630 635 640

Pro Thr Leu Ala Asn Ala Asp Trp Ile Gly Lys Thr Gly Thr Thr Asn 645 650 655

Gln Asp Glu Asn Met Trp Leu Met Leu Ser Thr Pro Arg Leu Thr Leu 660 665 670

Gly Gly Trp Ile Gly His Asp Asp Asn His Ser Leu Ser Arg Arg Ala 675 680 685

Gly Tyr Ser Asn Asn Ser Asn Tyr Met Ala His Leu Val Asn Ala Ile 690 695 700

Gln Gln Ala Ser Pro Ser Ile Trp Gly Asn Glu Arg Phe Ala Leu Asp 705 710 715 720

Pro Ser Val Val Lys Ser Glu Val Leu Lys Ser Thr Gly Gln Lys Pro 725 730 735

Glu Lys Val Ser Val Glu Gly Lys Glu Val Glu Val Thr Gly Ser Thr 740 745 750

Val Thr Ser Tyr Trp Ala Asn Lys Ser Gly Ala Pro Ala Thr Ser Tyr 755 760 765

Arg Phe Ala Ile Gly Gly Ser Asp Ala Asp Tyr Gln Asn Ala Trp Ser 770 775 780

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<213> Streptococcus pneumoniae

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Leu Phe Lys Lys Leu Arg Val His Tyr Thr Arg Ser Asp Val Glu Gln 50 55 60

Ile Gln Tyr Val Asn His Gln Ala Glu Glu Ser Leu Thr Ala Leu Leu 65 70 75 80

Glu Gln Met Pro Val Gly Val Met Lys Leu Asn Leu Ser Ser Gly Glu 85 90 95

Val Glu Trp Phe Asn Pro Tyr Ala Glu Leu Ile Leu Thr Lys Glu Asp 100 105 110

Gly Asp Phe Asp Leu Glu Ala Val Gln Thr Ile Ile Lys Ala Ser Val

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Phe Pro Asp Asn Ala Val Ile Thr Tyr Ile Glu Ser Gly Ala Ser Ser 455 450 Ala Ser Glu Leu Val Thr Glu Leu Ile Gln Phe Gln Asn Ser Lys Lys 475 470 Asn Arg Leu Ser Arg Met Gln Ala Ser Val Leu Met Ala Gly Met Met 490 485 Leu Asp Thr Lys Asn Phe Thr Ser Arg Val Thr Ser Arg Thr Phe Asp 505 Val Ala Ser Tyr Leu Arg Thr Arg Gly Ser Asp Ser Ile Ala Ile Gln 520 Glu Ile Ala Ala Thr Asp Phe Glu Glu Tyr Arg Glu Val Asn Glu Leu 535 Ile Leu Gln Gly Arg Lys Leu Gly Ser Asp Val Leu Ile Ala Glu Ala 555 545 Lys Asp Met Lys Cys Tyr Asp Thr Val Val Ile Ser Lys Ala Ala Asp 570 565 Ala Met Leu Ala Met Ser Gly Ile Glu Ala Ser Phe Val Leu Ala Lys 585 580 Asn Thr Gln Gly Phe Ile Ser Ile Ser Ala Arg Ser Arg Ser Lys Leu 600 Asn Val Gln Arg Ile Met Glu Glu Leu Gly Gly Gly His Phe Asn 615 610 Leu Ala Ala Gln Ile Lys Asp Val Thr Leu Ser Glu Ala Gly Glu 630 625 Lys Leu Thr Glu Ile Val Leu Asn Glu Met Lys Glu Lys Glu Lys Glu 650 645 Glu <210> 125 <211> 663 <212> DNA <213> Streptococcus pneumoniae <400> 125 atgaagtgct tgttatgtgg gcagactatg aagactgttt taacttttag tagtctctta 60 cttctgagga atgatgactc ttgtctttgt tcagactgtg attctacttt tgaaagaatt 120

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gcagcaggct ttgagtatct ggatttatta gagaaaagag aagagagagc cagttcttct 480 aaaaatcgtt cagagcgctt ggggacagaa cttcctttct ttattaaaag tggagtcact 540 attectaaaa aaateetaet tatagatgat atetataeta caggageaae tataaategt 600 gttaagaaac tgttggaaga agctggtgct aaggatgtaa aaacattttc ccttgtaaga 660 tga <210> 126 <211> 220 <212> PRT <213> Streptococcus pneumoniae <400> 126 Met Lys Cys Leu Leu Cys Gly Gln Thr Met Lys Thr Val Leu Thr Phe Ser Ser Leu Leu Leu Arg Asn Asp Asp Ser Cys Leu Cys Ser Asp 25 Cys Asp Ser Thr Phe Glu Arg Ile Gly Glu Glu Asn Cys Pro Asn Cys 45 40 Met Lys Thr Glu Leu Ser Thr Lys Cys Gln Asp Cys Gln Leu Trp Cys 55 Lys Glu Gly Val Glu Val Ser His Arg Ala Ile Phe Thr Tyr Asn Gln 75 70 Ala Met Lys Asp Phe Phe Ser Arg Tyr Lys Phe Asp Gly Asp Phe Leu Leu Arg Lys Val Phe Ala Ser Phe Leu Ser Glu Glu Leu Lys Lys Tyr 105 Lys Glu Tyr Gln Phe Val Val Ile Pro Leu Ser Pro Asp Arg Tyr Ala 120 Asn Arg Gly Phe Asn Gln Val Glu Gly Leu Val Glu Ala Ala Gly Phe 135 130 Glu Tyr Leu Asp Leu Leu Glu Lys Arg Glu Glu Arg Ala Ser Ser Ser 155 150 Lys Asn Arg Ser Glu Arg Leu Gly Thr Glu Leu Pro Phe Phe Ile Lys 165 Ser Gly Val Thr Ile Pro Lys Lys Ile Leu Leu Ile Asp Asp Ile Tyr 185 180 Thr Thr Gly Ala Thr Ile Asn Arg Val Lys Lys Leu Leu Glu Glu Ala 200 Gly Ala Lys Asp Val Lys Thr Phe Ser Leu Val Arg

215

210

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<210> 127

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- Met Ile Tyr Gln Val Val Ala Lys Val Ile Asn Ala Gly Gly Ala Val 130 135 140
- Cys Leu Ala Ser Pro Arg Ile Asp Val Cys Leu Glu Leu Tyr Lys Arg 145 150 155 160
- Leu Gln Gln Asp Phe Ser Cys Gly Ile Ala Leu Leu His Gly Glu Ser 165 170 175
- Glu Pro Tyr Phe Arg Thr Pro Leu Val Val Ala Thr Thr His Gln Leu 180 185 190
- Leu Lys Phe Tyr Gln Ala Phe Asp Leu Leu Ile Val Asp Glu Val Asp 195 200 205
- Ala Phe Pro Tyr Val Asp Asn Pro Met Leu Tyr His Ala Val Lys Asn 210 215 220
- Ser Val Lys Glu Asn Gly Leu Arg Ile Phe Leu Thr Ala Thr Ser Thr 225 230 235 240
- Asn Glu Leu Asp Lys Lys Val Arg Leu Gly Glu Leu Lys Arg Leu Asn 245 250 255
- Leu Pro Arg Arg Phe His Gly Asn Pro Leu Ile Ile Pro Lys Pro Ile 260 265 270
- Trp Leu Ser Asp Phe Asn Arg Tyr Leu Asp Lys Asn Arg Leu Ser Pro 275 280 285
- Lys Leu Lys Ser Tyr Ile Glu Lys Gln Arg Lys Thr Ala Tyr Pro Leu
- Leu Ile Phe Ala Ser Glu Ile Lys Lys Gly Glu Gln Leu Ala Glu Ile 305 310 315 320
- Leu Gln Glu Gln Phe Pro Asn Glu Lys Ile Gly Phe Val Ser Ser Val 325 330 335
- Thr Glu Asp Arg Leu Glu Gln Val Gln Ala Phe Arg Asp Gly Glu Leu 340 345 350
- Thr Ile Leu Ile Ser Thr Thr Ile Leu Glu Arg Gly Val Thr Phe Pro 355 360 365
- Cys Val Asp Val Phe Val Val Glu Ala Asn His Arg Leu Phe Thr Lys 370 375 380
- Ser Ser Leu Ile Gln Ile Gly Gly Arg Val Gly Arg Ser Met Asp Arg
- Pro Thr Gly Asp Leu Leu Phe Phe His Asp Gly Leu Asn Ala Ser Ile 405 410 415

Lys Lys Ala Ile Lys Glu Ile Gln Met Met Asn Lys Glu Ala Gly Leu 425

<210> 129

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Glu Glu Glu Ile Ala Val Val Thr Val Pro Gly Ala Ser Ala Gly Ile 115 Ser Ala Leu Ile Ala Ser Gly Leu Ala Pro Gln Pro His Ile Phe Tyr 135 Gly Phe Leu Pro Arg Lys Ser Gly Gln Gln Lys Gln Phe Phe Gly Leu 155 145 Lys Lys Asp Tyr Pro Glu Thr Gln Ile Phe Tyr Glu Ser Pro His Arg 170 165 Val Ala Asp Thr Leu Glu Asn Met Leu Glu Val Tyr Gly Asp Arg Ser 185 180 Val Val Leu Val Arg Glu Leu Thr Lys Ile Tyr Glu Glu Tyr Gln Arg 200 Gly Thr Ile Ser Glu Leu Leu Glu Ser Ile Ala Glu Thr Pro Leu Lys 215 Gly Glu Cys Leu Leu Ile Val Glu Gly Ala Ser Gln Gly Val Glu Glu 230 225 Lys Asp Glu Glu Asp Leu Phe Val Glu Ile Gln Thr Arg Ile Gln Gln 250 245 Gly Val Lys Lys Asn Gln Ala Ile Lys Glu Val Ala Lys Ile Tyr Gln 265 260 Trp Asn Lys Ser Gln Leu Tyr Ala Ala Tyr His Asp Trp Glu Glu Lys 285 280 Gln <210> 131 <211> 345 <212> DNA <213> Streptococcus pneumoniae <400> 131 atgataaaga aaggaaaggg ctgttttatg gacaaaaaag aattatttga cgcgctggat 60 gatttttccc aacaattatt ggtaacctta gccgatgtgg aagccatcaa gaaaaatctc 120 aagagcctgg tagaggaaaa tacagctctt cgcttggaaa atagtaagtt gcgagaacgc 180 ttgggtgagg tggaagcaga tgctcctgtc aaggccaagc atgttcgcga aagtgtccgt 240 cgtatttacc gtgatggatt tcacgtatgt aatgattttt atggacaacg tcgagagcag 300 345 gacgaagaat gtatgttttg tgacgagttg ttatacaggg agtaa <210> 132 <211> 114 <212> PRT <213> Streptococcus pneumoniae

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20 25 30

Val Glu Val Leu Thr Thr Arg Glu Pro Gly Gly Val Leu Ile Gly Glu 35 40 45

Lys Ile Arg Glu Val Ile Leu Asp Pro Ser His Thr Gln Met Asp Ala 50 55 60

Lys Thr Glu Leu Leu Leu Tyr Ile Ala Ser Arg Arg Gln His Leu Val 65 70 75 80

Glu Lys Val Leu Pro Ala Leu Glu Ala Gly Lys Leu Val Ile Met Asp 85 90 95

Arg Phe Ile Asp Ser Ser Val Ala Tyr Gln Gly Phe Gly Arg Gly Leu 100 105 110

Asp Ile Glu Ala Ile Asp Trp Leu Asn Gln Phe Ala Thr Asp Gly Leu 115 120 125

Lys Pro Asp Leu Thr Leu Tyr Phe Asp Ile Glu Val Glu Glu Gly Leu 130 135 140

Ala Arg Ile Ala Ala Asn Ser Asp Arg Glu Val Asn Arg Leu Asp Leu 145 150 155 160

Glu Gly Leu Asp Leu His Lys Lys Val Arg Gln Gly Tyr Leu Ser Leu 165 170 175

Leu Asp Lys Glu Gly Asn Arg Ile Val Lys Ile Asp Ala Ser Leu Pro 180 185 190

Leu Glu Gln Val Val Glu Thr Thr Lys Ala Val Leu Phe Asp Gly Met 195 200 205

Gly Leu Ala Lys 210

<210> 135

<211> 474

<212> DNA

<213> Streptococcus pneumoniae

<400> 135

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<211> 124

<212> PRT

<213> Streptococcus pneumoniae

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1311

gtggtcggta aattggttca cttggataga ggttactacg gtttccatga gaagttggcg 1260

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<210> 140

<211> 436

<212> PRT

<213> Streptococcus pneumoniae

<400> 140

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1 5 10 15

Gly Gly Asp Asn Arg Leu Val Gly Ser Val Thr Ile Glu Gly Ala Lys
20 25 30

Asn Ala Val Leu Pro Leu Leu Ala Ala Thr Ile Leu Ala Ser Glu Gly 35 40 45

Lys Thr Val Leu Gln Asn Val Pro Ile Leu Ser Asp Val Phe Ile Met 50 55 60

Asn Gln Val Val Gly Gly Leu Asn Ala Lys Val Asp Phe Asp Glu Glu 65 70 75 80

Ala His Leu Val Lys Val Asp Ala Thr Gly Asp Ile Thr Glu Glu Ala 85 90 95

Pro Tyr Lys Tyr Val Ser Lys Met Arg Ala Ser Ile Val Val Leu Gly
100 105 110

Pro Ile Leu Ala Arg Val Gly His Ala Lys Val Ser Met Pro Gly Gly 115 120 125

Cys Thr Ile Gly Ser Arg Pro Ile Asp Leu His Leu Lys Gly Leu Glu 130 135 140

Ala Met Gly Val Lys Ile Ser Gln Thr Ala Gly Tyr Ile Glu Ala Lys 145 150 155 160

Ala Glu Arg Leu His Gly Ala His Ile Tyr Met Asp Phe Pro Ser Val 165 170 175

Gly Ala Thr Gln Asn Leu Met Met Ala Ala Thr Leu Ala Asp Gly Val 180 185 190

Thr Val Ile Glu Asn Ala Ala Arg Glu Pro Glu Ile Val Asp Leu Ala 195 200 205

Ile Leu Leu Asn Glu Met Gly Ala Lys Val Lys Gly Ala Gly Thr Glu 210 215 220

Thr Ile Thr Ile Thr Gly Val Glu Lys Leu His Gly Thr Thr His Asn 225 230 235 240

Val Val Gln Asp Arg Ile Glu Ala Gly Thr Phe Met Val Ala Ala Ala 245 250 255

Met Thr Gly Gly Asp Val Leu Ile Arg Asp Ala Val Trp Glu His Asn 260 265 270

Arg Pro Leu Ile Ala Lys Leu Leu Glu Met Gly Val Glu Val Ile Glu 280 275 Glu Asp Glu Gly Ile Arg Val Arg Ser Gln Leu Glu Asn Leu Lys Ala 295 Val His Val Lys Thr Leu Pro His Pro Gly Phe Pro Thr Asp Met Gln 315 310 Ala Gln Phe Thr Ala Leu Met Thr Val Ala Lys Gly Glu Ser Thr Met 330 325 Val Glu Thr Val Phe Glu Asn Arg Phe Gln His Leu Glu Glu Met Arg 345 Arg Met Gly Leu His Ser Glu Ile Ile Arg Asp Thr Ala Arg Ile Val 355 Gly Gly Gln Pro Leu Gln Gly Ala Glu Val Leu Ser Thr Asp Leu Arg 375 Ala Ser Ala Ala Leu Ile Leu Thr Gly Leu Val Ala Gln Gly Glu Thr 395 390 Val Val Gly Lys Leu Val His Leu Asp Arg Gly Tyr Tyr Gly Phe His 410 405 Glu Lys Leu Ala Gln Leu Gly Ala Lys Ile Gln Arg Ile Glu Ala Ser 425 Asp Glu Asp Glu 435 <210> 141 <211> 1101 <212> DNA <213> Streptococcus pneumoniae <400> 141 atgttattag cgtcaacagt agccttgtca tttgccccag tattggcaac tcaagcagaa 60 gaagttettt ggaetgeacg tagtgttgag caaateeaaa acgatttgae taaaaeggae 120 aacaaaacaa gttataccgt acagtatggt gatactttga gcaccattgc agaagccttg 180 ggtgtagatg tcacagtgct tgcgaatctg aacaaaatca ctaatatgga cttgattttc 240 ccagaaactg ttttgacaac gactgtcaat gaagcagaag aagtaacaga agttgaaatc 300 caaacacctc aagcagactc tagtgaagaa gtgacaactg cgacagcaga tttgaccact 360 aatcaagtga ccgttgatga tcaaactgtt caggttgcag acctttctca accaattgca 420 gaagttacaa agacagtgat tgcttctgaa gaagtggcac catctacggg cacttctgtc 480 ccagaggagc aaacgaccga aacaactcgc ccagttgcag aagaagctcc tcaggaaacg 540 actccagctg agaagcagga aacacaaaca agccctcaag ctgcatcagc agtggaagca 600 actacaacaa gttcagaagc aaaagaagta gcatcatcaa atggagctac agcagcagtt 660 tctacttatc aaccagaaga aacgaaagta atttcaacaa cttacgaggc tccagctgcg 720 cccgattatg ctggacttgc agtagcaaaa tctgaaaatg caggtcttca accacaaaca 780 gctgccttta agaagaaatt gctaacttgt ttggcattac atcctttagt ggttatcgtc 840 caggagacag tggagatcac ggaaaaggtt tggctatcga ctttatggta ccagaacgtt 900 cagaattagg ggataagatt gcggaatatg ctattcaaaa tatggccagc cgtggcatta 960 gttacatcat ctggaaacaa cgtttctatg ctccattcga tagcaaatat gggccagcta 1020 acacttggaa cccaatgcca gaccgtggta gtgtgacaga aaatcactat gatcacgttc 1080 acqtttcaat gaatggataa 1100

<210> 142

<211> 302

<212> PRT

<213> Streptococcus pneumoniae

<400> 142

Met Leu Leu Ala Ser Thr Val Ala Leu Ser Phe Ala Pro Val Leu Ala 1 5 10 15

Thr Gln Ala Glu Glu Val Leu Trp Thr Ala Arg Ser Val Glu Gln Ile 20 25 30

Gln Asn Asp Leu Thr Lys Thr Asp Asn Lys Thr Ser Tyr Thr Val Gln 35 40 45

Tyr Gly Asp Thr Leu Ser Thr Ile Ala Glu Ala Leu Gly Val Asp Val 50 55 60

Thr Val Leu Ala Asn Leu Asn Lys Ile Thr Asn Met Asp Leu Ile Phe 65 70 75 80

Pro Glu Thr Val Leu Thr Thr Thr Val Asn Glu Ala Glu Glu Val Thr 85 90 95

Glu Val Glu Ile Gln Thr Pro Gln Ala Asp Ser Ser Glu Glu Val Thr

Thr Ala Thr Ala Asp Leu Thr Thr Asn Gln Val Thr Val Asp Asp Gln 115 120 125

Thr Val Gln Val Ala Asp Leu Ser Gln Pro Ile Ala Glu Val Thr Lys 130 135 140

Thr Val Ile Ala Ser Glu Glu Val Ala Pro Ser Thr Gly Thr Ser Val 145 150 155 160

Pro Glu Glu Gln Thr Thr Glu Thr Thr Arg Pro Val Ala Glu Glu Ala 165 170 175

Pro Gln Glu Thr Thr Pro Ala Glu Lys Gln Glu Thr Gln Thr Ser Pro 180 185 190

Gln Ala Ala Ser Ala Val Glu Ala Thr Thr Thr Ser Ser Glu Ala Lys 195 200 205

Glu Val Ala Ser Ser Asn Gly Ala Thr Ala Ala Val Ser Thr Tyr Gln 210 215 220

Pro Glu Glu Thr Lys Val Ile Ser Thr Thr Tyr Glu Ala Pro Ala Ala

225 230 235 240

Pro Asp Tyr Ala Gly Leu Ala Val Ala Lys Ser Glu Asn Ala Gly Leu 245 250 255

Gln Pro Gln Thr Ala Ala Phe Lys Lys Lys Leu Leu Thr Cys Leu Ala 260 265 270

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- Asn Ile Ile Thr Ile Tyr Gln Ala Ile Phe Ile Ala Leu Gly Ala Ala 50 55 60
- Ile Ser Ser Val Ile Ser Lys Ser Ile Gly Gln Lys Asp Gln Ser Lys 65 70 75 80
- Leu Ala Tyr His Val Thr Glu Ala Leu Lys Ile Thr Leu Leu Leu Ser 85 90 95
- Phe Leu Leu Gly Phe Leu Ser Ile Phe Ala Gly Lys Glu Met Ile Gly
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- Leu Leu Gly Thr Glu Arg Asp Val Ala Glu Ser Gly Gly Leu Tyr Leu 115 120 125
- Ser Leu Val Gly Gly Ser Ile Val Leu Leu Gly Leu Met Thr Ser Leu 130 135 140
- Gly Ala Leu Ile Arg Ala Thr His Asn Pro Arg Leu Pro Leu Tyr Val 145 150 155 160
- Ser Phe Leu Ser Asn Ala Leu Asn Ile Leu Phe Ser Ser Leu Ala Ile 165 170 175
- Phe Val Leu Asp Met Gly Ile Ala Gly Val Ala Trp Gly Thr Ile Val
- Ser Arg Leu Val Gly Leu Val Ile Leu Trp Ser Gln Leu Lys Leu Pro
- Tyr Gly Lys Pro Thr Phe Gly Leu Asp Lys Glu Leu Leu Thr Leu Ala 210 215 220
- Leu Pro Ala Ala Gly Glu Arg Leu Met Met Arg Ala Gly Asp Val Val 225 230 235 240
- Ile Ile Ala Leu Val Val Ser Phe Gly Thr Glu Ala Val Ala Gly Asn 245 250 255
- Ala Ile Gly Glu Val Leu Thr Gln Phe Asn Tyr Met Pro Ala Phe Gly 260 265 270
- Val Ala Thr Ala Thr Val Met Leu Leu Ala Arg Ala Val Gly Glu Asp 275 280 285
- Asp Trp Lys Arg Val Ala Ser Leu Ser Lys Gln Thr Phe Trp Leu Ser 290 295 300
- Leu Phe Leu Met Leu Pro Leu Ser Phe Ser Ile Tyr Val Leu Gly Val 305 310 315 320
- Pro Leu Thr His Leu Tyr Thr Thr Asp Ser Leu Ala Val Glu Ala Ser 325 330 335

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35 40 45

Glu Ser Asp Leu Ala Val Ser Arg Phe Phe Glu Ile Leu Asp Asn Ile 50 55 60

His Val Thr Ile Glu Asn Phe Met Asp Lys Ala Arg Asn Phe His Asn 65 70 75 80

His Glu His Val Ser Met Met Ala Gln Ile Ile Pro Leu Tyr Tyr Ser 85 90 95

Asn Asp Ile Ala Gly Phe Gln Lys Leu Gln Arg Glu Gln Leu Glu Lys
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Ser Lys Ser Ser Thr Thr Pro Leu Tyr Phe Glu Leu Asn Trp Ile Leu 115 120 125

Leu Gln Gly Leu Ile Cys Gln Arg Asp Ala Ser Tyr Asp Met Lys Gln 130 135 140

Asp Asp Leu Gly Lys Val Ala Asp Tyr Leu Phe Lys Thr Glu Glu Trp 145 150 155 160

Thr Met Tyr Glu Leu Ile Leu Phe Gly Asn Leu Tyr Ser Phe Tyr Asp 165 170 175

Val Asp Tyr Val Thr Arg Ile Gly Arg Glu Val Met Glu Arg Glu Glu 180 185 190

Phe Tyr Gln Glu Ile Ser Arg His Lys Arg Leu Val Leu Ile Leu Ala 195 200 205

Leu Asn Cys Tyr Gln His Cys Leu Glu His Ser Ser Phe Tyr Asn Ala 210 215 220

Asn Tyr Phe Glu Ala Tyr Thr Glu Lys Ile Ile Asp Lys Gly Ile Lys 225 230 235 240

Leu Tyr Glu Arg Asn Val Phe His Tyr Leu Lys Gly Phe Ala Leu Tyr 245 250 255

Gln Lys Gly Gln Cys Lys Glu Gly Cys Lys Gln Met Gln Glu Ala Met 260 265 270

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1068

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Lys Thr Thr Thr Ser Ile Asn Ile Ala Trp Ser Phe Ala Arg Ala Gly 50 55 60

Tyr Lys Thr Leu Leu Ile Asp Gly Asp Thr Arg Asn Ser Val Met Leu 65 70 75 80

Gly Val Phe Lys Ser Arg Glu Lys Ile Thr Gly Leu Thr Glu Phe Leu 85 90 95

Ser Gly Thr Ala Asp Leu Ser His Gly Leu Cys Asp Thr Asn Ile Glu

Asn Leu Phe Val Val Gln Ser Gly Ser Val Ser Pro Asn Pro Thr Ala

Leu Leu Gln Ser Lys Asn Phe Asn Asp Met Ile Glu Thr Leu Arg Lys

Tyr Phe Asp Tyr Ile Ile Ile Asp Thr Pro Pro Ile Gly Ile Val Ile 145 150 155 160

Asp Ala Ala Ile Ile Thr Gln Lys Cys Asp Ala Ser Ile Leu Val Thr

Ala Thr Gly Glu Ala Asn Lys Arg Asp Ile Gln Lys Ala Lys Gln Gln
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125

120

Asn Gly Ala Ser Lys Val Asp Ile Arg Leu Ser Asp Gly Thr Lys Val 130 135 140

Pro Gly Glu Ile Val Gly Ala Asp Thr Phe Ser Asp Ile Ala Val Val 145 150 155 160

Lys Ile Ser Ser Glu Lys Val Thr Thr Val Ala Glu Phe Gly Asp Ser 165 170 175

Ser Lys Leu Thr Val Gly Glu Thr Ala Ile Ala Ile Gly Ser Pro Leu 180 185 190

Gly Ser Glu Tyr Ala Asn Thr Val Thr Gln Gly Ile Val Ser Ser Leu 195 200 205

Asn Arg Asn Val Ser Leu Lys Ser Glu Asp Gly Gln Ala Ile Ser Thr 210 215 220

Lys Ala Ile Gln Thr Asp Thr Ala Ile Asn Pro Gly Asn Ser Gly Gly 225 230 235 240

Pro Leu Ile Asn Ile Gln Gly Gln Val Ile Gly Ile Thr Ser Ser Lys 245 250 255

Ile Ala Thr Asn Gly Gly Thr Ser Val Glu Gly Leu Gly Phe Ala Ile 260 265 270

Pro Ala Asn Asp Ala Ile Asn Ile Ile Glu Gln Leu Glu Lys Asn Gly 275 280 285

Lys Val Thr Arg Pro Ala Leu Gly Ile Gln Met Val Asn Leu Ser Asn 290 295 300

Val Ser Thr Ser Asp Ile Arg Arg Leu Asn Ile Pro Ser Asn Val Thr 305 310 315 320

Ser Gly Val Ile Val Arg Ser Val Gln Ser Asn Met Pro Ala Asn Gly 325 330 335

His Leu Glu Lys Tyr Asp Val Ile Thr Lys Val Asp Asp Lys Glu Ile 340 345 350

Ala Ser Ser Thr Asp Leu Gln Ser Ala Leu Tyr Asn His Ser Ile Gly 355 360 365

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Leu Ile Asp Ala Ala Asn Tyr Glu Lys Pro Ser Gln Glu Val Leu Lys 165 Ala Ser Leu Ser Glu Glu Ser Tyr Arg Val Thr Gln Glu Ala Ala Thr 185 180 Glu Ala Pro Phe Thr Asn Ala Tyr Asp Gln Thr Phe Glu Glu Gly Ile 200 195 Tyr Val Asp Ile Thr Thr Gly Glu Pro Leu Phe Phe Ala Lys Asp Lys 215 Phe Ala Ser Gly Cys Gly Trp Pro Ser Phe Ser Arg Pro Ile Ser Lys 235 230 Glu Leu Ile His Tyr Tyr Lys Asp Leu Ser His Gly Met Glu Arg Ile 250 245 Glu Val Arg Ser Arg Ser Gly Ser Ala His Leu Gly His Val Phe Thr 265 Asp Gly Pro Arg Glu Leu Gly Gly Leu Arg Tyr Cys Ile Asn Ser Ala 280 Ser Leu Arg Phe Val Ala Lys Asp Glu Met Glu Lys Ala Gly Tyr Gly 295 290 Tyr Leu Leu Pro Tyr Leu Asn Lys 310 305 <210> 155 <211> 870 <212> DNA <213> Streptococcus pneumoniae <400> 155 atgaagatta ttgtacctgc aaccagtgcc aatatcgggc caggttttga ctcggtcggt 60 qtaqctgtaa ccaagtatct tcaaattgag gtctgcgaag aacgagatga gtggctgatt 120 gaacaccaga ttggcaaatg gattccacat gacgagcgta atctcttgct caaaatcgct 180 ttgcaaattg taccagactt gcaaccaaga cgcttgaaaa tgaccagtga tgtccctttg 240 gegegeggtt tgggttette eageteggtt ategttgetg ggattgaact agecaaccaa 300 ctqqqtcaac tcaacttatc agaccatgaa aaattgcagt tagcgaccaa gattgaaggg 360 catcctgaca atgtggctcc agccatttat ggtaatctcg ttattgcaag ttctgttgaa 420 gggcaagtct ctgctatcgt agcagacttt ccagagtgtg attttctagc ttacattcca 480 aactatgaat tacgtactcg cgacagccgt agtgtcttgc ctaaaaaatt gtcttataag 540 gaagetgttg etgeaagtte tategeeaat gtageggttg etgeettgtt ggeaggagae 600 atggtgaccg ctgggcaagc aatcgaggga gacctcttcc atgagcgcta tcgtcaggac 660 ttggtaagag aatttgcgat gattaagcaa gtgaccaaag aaaatggggc ctatgcaacc 720 tacctttctg gtgctgggcc gacagttatg gttctggctt ctcatgacaa gatgccaaca 780 attaaggcag aattggaaaa gcaacctttc aaaggaaaac tgcatgactt gagagttgat 840 870 acccaaggtg tccgtgtaga agcaaaataa <210> 156

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Pro His Asp Glu Arg Asn Leu Leu Leu Lys Ile Ala Leu Gln Ile Val 50 55 60

Pro Asp Leu Gln Pro Arg Arg Leu Lys Met Thr Ser Asp Val Pro Leu 65 70 75 80

Ala Arg Gly Leu Gly Ser Ser Ser Val Ile Val Ala Gly Ile Glu 85 90 95

Leu Ala Asn Gln Leu Gly Gln Leu Asn Leu Ser Asp His Glu Lys Leu 100 105 110

Gln Leu Ala Thr Lys Ile Glu Gly His Pro Asp Asn Val Ala Pro Ala 115 120 125

Ile Tyr Gly Asn Leu Val Ile Ala Ser Ser Val Glu Gly Gln Val Ser 130 135 140

Ala Ile Val Ala Asp Phe Pro Glu Cys Asp Phe Leu Ala Tyr Ile Pro 145 150 155 160

Asn Tyr Glu Leu Arg Thr Arg Asp Ser Arg Ser Val Leu Pro Lys Lys 165 170 175

Leu Ser Tyr Lys Glu Ala Val Ala Ala Ser Ser Ile Ala Asn Val Ala 180 185 190

Val Ala Ala Leu Leu Ala Gly Asp Met Val Thr Ala Gly Gln Ala Ile 195 200 205

Glu Gly Asp Leu Phe His Glu Arg Tyr Arg Gln Asp Leu Val Arg Glu 210 215 220

Phe Ala Met Ile Lys Gln Val Thr Lys Glu Asn Gly Ala Tyr Ala Thr 225 230 235 240

Tyr Leu Ser Gly Ala Gly Pro Thr Val Met Val Leu Ala Ser His Asp 245 250 255

Lys Met Pro Thr Ile Lys Ala Glu Leu Glu Lys Gln Pro Phe Lys Gly 260 265 270

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• . . jai

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- Pro Lys Asp Leu Asn Arg Tyr Thr Ala Glu Ser Val Thr Ala Val Lys
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- Glu Ala Glu Lys Ala Ile Arg Ser Leu Asp Ser Asn Leu Ser Arg Ala 595 600 605
- Gln Gln Asp Thr Ile Asp Gln Ala Ile Ala Lys Leu Gln Glu Thr Val 610 615 620
- Asn Asn Leu Thr Leu Thr Pro Glu Ala Gln Lys Glu Glu Glu Ala Lys 625 630 635 640
- Arg Glu Val Glu Lys Leu Ala Lys Asn Lys Val Ile Ser Ile Asp Ala 645 650 655
- Gly Arg Lys Tyr Phe Thr Leu Asn Gln Leu Lys Arg Ile Val Asp Lys 660 665 670
- Ala Ser Glu Leu Gly Tyr Ser Asp Val His Leu Leu Leu Gly Asn Asp 675 680 685
- Gly Leu Arg Phe Leu Leu Asp Asp Met Thr Ile Thr Ala Asn Gly Lys 690 695 700
- Thr Tyr Ala Ser Asp Asp Val Lys Lys Ala Ile Ile Glu Gly Thr Lys 705 710 715 720
- Ala Tyr Tyr Asp Asp Pro Asn Gly Thr Ala Leu Thr Gln Ala Glu Val
 725 730 735
- Thr Glu Leu Ile Glu Tyr Ala Lys Ser Lys Asp Ile Gly Leu Ile Pro
 740 745 750
- Ala Ile Asn Ser Pro Gly His Met Asp Ala Met Leu Val Ala Met Glu
 755 760 765
- Lys Leu Gly Ile Lys Asn Pro Gln Ala His Phe Asp Lys Val Ser Lys
 770 780
- Thr Thr Met Asp Leu Lys Asn Glu Glu Ala Met Asn Phe Val Lys Ala
 785 790 795 800
- Leu Ile Gly Lys Tyr Met Asp Phe Phe Ala Gly Lys Thr Lys Ile Phe 805 810 815
- Asn Phe Gly Thr Asp Glu Tyr Ala Asn Asp Ala Thr Ser Ala Gln Gly 820 825 830

- Trp Tyr Tyr Leu Lys Trp Tyr Gln Leu Tyr Gly Lys Phe Ala Glu Tyr
- Ala Asn Thr Leu Ala Ala Met Ala Lys Glu Arg Gly Leu Gln Pro Met 850 855 860
- Ala Phe Asn Asp Gly Phe Tyr Tyr Glu Asp Lys Asp Asp Val Gln Phe 865 870 875 886
- Asp Lys Asp Val Leu Ile Ser Tyr Trp Ser Lys Gly Trp Trp Gly Tyr 885 890 895
- Asn Leu Ala Ser Pro Gln Tyr Leu Ala Ser Lys Gly Tyr Lys Phe Leu 900 905 910
- Asn Thr Asn Gly Asp Trp Tyr Tyr Ile Leu Gly Gln Lys Pro Glu Asp 915 920 925
- Gly Gly Gly Phe Leu Lys Lys Ala Ile Glu Asn Thr Gly Lys Thr Pro 930 935 940
- Phe Asn Gln Leu Ala Ser Thr Lys Tyr Pro Glu Val Asp Leu Pro Thr 945 950 955 960
- Val Gly Ser Met Leu Ser Ile Trp Ala Asp Arg Pro Ser Ala Glu Tyr 965 970 975
- Lys Glu Glu Glu Ile Phe Glu Leu Met Thr Ala Phe Ala Asp His Asn 980 985 990
- Lys Asp Tyr Phe Arg Ala Asn Tyr Asn Ala Leu Arg Glu Glu Leu Ala 995 1000 1005
- Lys Ile Pro Thr Asn Leu Glu Gly Tyr Ser Lys Glu Ser Leu Glu Ala 1010 1015 1020
- Leu Asp Ala Ala Lys Thr Ala Leu Asn Tyr Asn Leu Asn Arg Asn Lys 1025 1030 1035 1040
- Gln Ala Glu Leu Asp Thr Leu Val Ala Asn Leu Lys Ala Ala Leu Gln 1045 1050 1055
- Gly Leu Lys Pro Ala Val Thr His Ser Gly Ser Leu Asp Glu Asn Glu 1060 1065 1070
- Val Ala Ala Asn Val Glu Thr Arg Pro Glu Leu Ile Thr Arg Thr Glu 1075 1080 1085
- Glu Ile Pro Phe Glu Val Ile Lys Lys Glu Asn Pro Asn Leu Pro Ala 1090 1095 1100
- Gly Gln Glu Asn Ile Ile Thr Ala Gly Val Lys Gly Glu Arg Thr His 1105 1110 1115 1120
- Tyr Ile Ser Val Leu Thr Glu Asn Gly Lys Thr Thr Glu Thr Val Leu 1125 1130 1135

Asp Ser Gln Val Thr Lys Glu Val Ile Asn Gln Val Val Glu Val Gly 1140 1145 1150

Ala Pro Val Thr His Lys Gly Asp Glu Ser Gly Leu Ala Pro Thr Thr

Glu Val Lys Pro Arg Leu Asp Ile Gln Glu Glu Glu Ile Pro Phe Thr 1170 1175 1180

Thr Val Thr Cys Glu Asn Pro Leu Leu Leu Lys Gly Lys Thr Gln Val

Ile Thr Lys Gly Val Asn Gly His Arg Ser Asn Phe Tyr Ser Val Ser 1205 1210 1215

Thr Ser Ala Asp Gly Lys Glu Val Lys Thr Leu Val Asn Ser Val Val 1220 1225 1230

Ala Gln Glu Ala Val Thr Gln Ile Val Glu Val Gly Thr Met Val Thr 1235 1240 1245

His Val Gly Asp Glu Asn Gly Gln Ala Ala Ile Ala Glu Glu Lys Pro 1250 1260

Lys Leu Glu Ile Pro Ser Gln Pro Ala Pro Ser Thr Ala Pro Ala Glu 1265 1270 1275 1280

Glu Ser Lys Val Leu Pro Gln Asp Pro Ala Pro Val Val Thr Glu Lys 1285 1290 1295

Lys Leu Pro Glu Thr Gly Thr His Asp Ser Ala Gly Leu Val Val Ala 1300 1305 1310

Gly Leu Met Ser Thr Leu Ala Ala Tyr Gly Leu Thr Lys Arg Lys Glu 1315 1320 1325

Asp

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<212> DNA

<213> Streptococcus pneumoniae

<400> 167

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Leu Leu Gly Tyr Ala Leu Ile Gly Gly Leu Asp Gly Phe Asp Ala Ser

165 170 175

Thr Ser Asn Pro Lys Asn Ile Ala Val Gln Thr Ala Trp Ala Asn Gln 180 185 190

Ala Gln Ala Glu Tyr Ser Thr Gly Gln Asn Tyr Tyr Glu Ser Lys Val 195 200 205

Arg Lys Ala Leu Asp Gln Asn Lys Arg Val Arg Tyr Arg Val Thr Leu 210 215 220

Tyr Tyr Ala Ser Asn Glu Asp Leu Val Pro Ser Ala Ser Gln Ile Glu 225 230 235 240 Ala Lys Ser Ser Asp Gly Glu Leu Glu Phe Asn Val Leu Val Pro Asn 250 245 Val Gln Lys Gly Leu Gln Leu Asp Tyr Arg Thr Gly Glu Val Thr Val 265 260 Thr Gln <210> 169 <211> 225 <212> DNA <213> Streptococcus pneumoniae <400> 169 gtgctaagat tcagcggatt gaggcaagtg atgaagatga ataagaaatc aagctacgta 60 gtcaagcgtt tacttttagt catcatagta ctgattttag gtactctggc tctaggaatc 120 ggtttaatgg taggttatgg aatcttgggc aagggtcaag atccatgggc tatcctgtct 180 225 ccagcaaaat ggcaggaatt gattcataaa tttacaggaa attag <210> 170 <211> 74 <212> PRT <213> Streptococcus pneumoniae <400> 170 Val Leu Arg Phe Ser Gly Leu Arg Gln Val Met Lys Met Asn Lys Lys Ser Ser Tyr Val Val Lys Arg Leu Leu Leu Val Ile Ile Val Leu Ile Leu Gly Thr Leu Ala Leu Gly Ile Gly Leu Met Val Gly Tyr Gly Ile Leu Gly Lys Gly Gln Asp Pro Trp Ala Ile Leu Ser Pro Ala Lys Trp 55 Gln Glu Leu Ile His Lys Phe Thr Gly Asn 70 65 <210> 171 <211> 40 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: Primer

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<400> 171

cgagatctga tatctcacaa acagataacg gcgtaaatag

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<220>
<223> Description of Artificial Sequence: Primer
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gaagatette ecegggatea caaacagata aeggegtaaa tag
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<211> 42
<212> DNA
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<223> Description of Artificial Sequence: Primer
cgagatctga tatccatcac aaacagataa cggcgtaaat ag
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<211> 32
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<211> 23
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ggatgctttg tttcaggtgt atc -
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| <400> 177 gcggatcccc cgggcttaat taatgtttaa acactagtcg aagatctcgc gaattctcct gtgtgaaatt gttatccgct a | 60 81 |
| <210> 178 <211> 24 <212> DNA <213> Artificial Sequence | |
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| <400> 179 tcaggggggc ggagcctatg | 20 |
| <210> 180 <211> 22 <212> DNA <213> Artificial Sequence | |
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| <400> 180 tcgtatgttg tgtggaattg tg | 22 |
| <210> 181 <211> 26 <212> DNA | |

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<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Primer
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tccggctcgt atgttgtgtg gaattg
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<221> SITE
<222> (3)
<223> Xaa=Any amino acid
<220>
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      anchoring motif
<400> 182
Leu Pro Xaa Thr Gly
<210> 183
<211> 18
<212> DNA
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<211> 10
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<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Primer
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                                                                     10
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 <211> 43
 <212> DNA
 <213> Artificial Sequence
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| <210> 187 <211> 36 <212> DNA <213> Artificial Sequence | |
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| <210> 188 <211> 38 <212> DNA <213> Artificial Sequence | |
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| <400> 188 ccctcgaggg ctacttccga tacattttaa actgtagg | 38 |
| <210> 189 <211> 35 <212> DNA <213> Artificial Sequence | |
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| <210> 190 | |

| <211> 32 | |
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| <210> 191 | |
| <211> 38 | |
| <212> DNA | |
| <213> Artificial Sequence | |
| <220> | |
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| <210> 192 | |
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| <212> DNA | |
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| tigeggeege acceedate teaatesses | |
| <210> 193 | |
| <211> 40 | |
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| <213> Artificial Sequence | |
| <220> | |
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| <210> 194 | |
| <211> 32 | |
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| <400> 194 | 32 |
| | |

<210> 195

<211> 48

<212> PRT

<213> Streptococcus pneumoniae

<400> 195

Gly Ile Arg Leu Arg Asn Met Leu Phe Lys Ile Trp Pro Ala Val Ala 1 5 10 15

Leu Val Thr Ser Ser Gly Asn Asn Val Ser Met Leu His Ser Ile Ala 20 25 30

Asn Met Gly Gln Leu Thr Leu Gly Thr Gln Cys Gln Thr Val Val Val 35 40 45

<210> 196

<211> 11

<212> PRT

<213> Streptococcus pneumoniae

<400> 196

Gln Lys Ile Thr Met Ile Thr Phe Thr Phe Gln
1 5 10